

# SEQUENCE LISTING

<110> Rozzell, J. David  
Bui, Peter  
Hua, Ling

<120> SYNTHETIC GENES FOR ENHANCED EXPRESSION

<130> B583:40608

<150> 09/494,921

<151> 2000-01-31

<160> 79

<170> PatentIn version 3.0

<210> 1

<211> 1197

<212> DNA

<213> Pseudomonas putida

<400> 1

```
atgcacggct ccaacaagct ccaggattt gccacccgcg ccattcacca tggctacgac      60
ccccaggacc acggcggcgc actggtgcc a cgggtctacc agaccgcgac gttcaccttc      120
cccaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggccgggca tttctacagc      180
cgcattctcca accccaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc      240
gaggccgggc tggcgtggtc ctccggcatg ggggcgatca cgtccacgct atggacactg      300
ctgcgccccg gtgacgaggt gctgctgggc aacacctgt acggctgcac ctttgcttc      360
ctgcaccacg gcatcggcga gttcggggtc aagctgcgcc atgtggacat ggccgacctg      420
caggcactgg aggcggccat gacgcgggcc acccggtga tctatttcga gtcgcgggcc      480
aaccccaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc      540
gcgaccgtgg tggtcgacaa cacctactgc acgcggtacc tgcaacggcc actggagctg      600
ggcgccgacc tgggtggtgca ttccggccacc aagtacctga gcggccatgg cgacatcact      660
gctggcattg tgggtgggcag ccaggcactg gtggaccgta tacgtctgca gggcctcaag      720
gacatgaccg gtgcggtgct ctgcgcccat gacgcgcgac tgttgatgcg cggcatcaag      780
accctcaacc tgcgcatgga ccgccactgc gccaacgctc aggtgctggc cgagttcctc      840
gcccggcagc cgcagggtga gctgatccat taccggggcc tggcgagctt cccgcagtac      900
accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc      960
ggcatcggtg ccgggcggcg gttcatgaac gccctgcaac tgttcagccg cgcggtgagc     1020
ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc     1080
ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcggttgtc ggtggggctg     1140
```









[illegible]

```
<210> 7
<211> 430
<212> DNA
<213> Artificial sequence
```

```
<210> 8
<211> 366
<212> DNA
<213> Artificial sequence
```

5

<210> 9  
 <211> 383  
 <212> DNA  
 <213> Artificial sequence  
  
 <400> 9  
 tcttaatgaa ttcttggtc gtcagccgca ggtagaactg atccactatc cgggcctggc 60  
 ttccttcccg cagtacactc tggcacgtca gcagatgtcc cagccgggcg gtatgatcgc 120  
 tttcgaactg aaggggtggca tcggcgctgg tcgtcgtttc atgaacgctc tgcagctggt 180  
 ctcccgctgc gtttccttgg gtgacgtga atccctggcg cagcaccgag catccatgac 240  
 tcactcctcc tacactccgg aagaacgtgc gcactacggc atctccgaag gcttggttcg 300  
 tctgtctgtt ggtctggaag acatcgatga tctgctggca gacgttcagc aggctctgaa 360  
 ggctagcgct tgaggatcca cca 383

<210> 10  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 10  
 caagaggcca tgggtcacgg ctccaacaaa ctg 33

<210> 11  
 <211> 114  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 11  
 cacggctcca acaaactgcc gggctttgct accgcgcta tccaccacgg ttatgaccgg 60  
 caggatcacg gtggtgcact ggttcgcgcg gttaccaga ctgctacttt cacc 114

<210> 12  
 <211> 116  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 12  
 gcttcagca ggttcagggt cgggttgag atacgggagt agaagtgacc agcctgttcg 60  
 ccagcaaagc acgcagcgcc gtattcaacg gtcgggaagg tgaaagtagc agtctg 116

<210> 13  
 <211> 117  
 <212> DNA  
 <213> Artificial Sequence  
  
 <400> 13  
 ctgaacctgc tggaagcacg tatggcatct ctggaaggcg gcgaagctgg tctggcgctg 60







accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc 960  
 ggcatcggtg ccgggcgctg ttatcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020  
 ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080  
 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tcggtttgtc ggtggggctg 1140  
 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgcttga 1197

<210> 29  
 <211> 1197  
 <212> DNA  
 <213> Artificial Sequence

<400> 29  
 atgcacggct ocaacaagct ccaggattt gccaccgcg ccattcacca tggctacgac 60  
 ccgcaggacc acggcggcgc actggtgcc aagggtctacc agaccgcgac gttcaccttc 120  
 ccgaccgtgg aatacggcgc tcggtgcttt gccggcgagc aggcggggca tttctacagc 180  
 cgcattctca acccgacct caacctgctg gaagcacgca tggcctcgct ggaaggcggc 240  
 gaggcggggc tggcgctggc ctggggcatg ggggcgatca cgtccacgct gtggacactg 300  
 ctgcgcccgg gtgacgaggt gctgctgggc aacacctgt acggctgcac ctttgcttc 360  
 ctgcaccacg gcacggcga gttcggggtc aagctgcgc atgtggacat ggccgacctg 420  
 caggcaactg aggcggccat gaagcgggc acccggtgta tctatttcga gtgcggggc 480  
 aaccgaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc 540  
 gcgaccgtgg tggtcgacaa cacctactgc acgccgtacc tgcaacgtcc actggagctg 600  
 gggcgcgacc tgggtggtgca ttccggccacc aagtacctga ggcggcatgg cgacatcact 660  
 gctggcattg tgggtggcag ccaggcactg gtggaccgta tccgtctgca gggcctcaag 720  
 gacatgaccg gtgcggtgct ctgcgcgat gacgcgcac tgttgatgcg cggcatcaag 780  
 accctcaacc tgcgcattga ccgcactgc gccaacgctc aggtgctggc cgagttcctc 840  
 gccgctcagc cgcagggtgga gctgatccat taccggggcc tggcgagctt cccgcagtac 900  
 accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc 960  
 ggcatcggtg ccgggcgctg ttatcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020  
 ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080  
 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tcggtttgtc ggtggggctg 1140  
 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgcttga 1197

<210> 30  
 <211> 1200  
 <212> DNA







Asn Phe Asp Ala Lys Met Val Asp Ala Ile Ile Glu Ala Thr Gly Val  
165 170 175

Thr Pro Ser Val Asn Gln Ile Glu Arg His Pro Leu Leu Leu Gln Pro  
180 185 190

Glu Leu Ile Ala His His Lys Ala Lys Asn Ile His Ile Thr Ala Tyr  
195 200 205

Ser Pro Leu Gly Asn Asn Thr Val Gly Ala Pro Leu Leu Val Gln His  
210 215 220

Pro Glu Ile Lys Arg Ile Ala Glu Lys Asn Gly Cys Thr Pro Ala Gln  
225 230 235 240

Val Leu Ile Ala Trp Ala Ile Val Gly Gly His Ser Val Ile Pro Lys  
245 250 255

Ser Val Thr Pro Ser Arg Ile Gly Glu Asn Phe Lys Gln Val Ser Leu  
260 265 270

Ser Gln Glu Asp Val Asp Ala Val Ser Lys Leu Gly Glu Gly Ser Gly  
275 280 285

Arg Arg Arg Tyr Asn Ile Pro Cys Thr Tyr Ser Pro Lys Trp Asp Ile  
290 295 300

Asn Val Phe Gly Glu Glu Asp Glu Lys Ser Cys Lys Asn Ala Val Lys  
305 310 315 320

Ile Lys

<210> 33  
<211> 972  
<212> DNA  
<213> Artificial sequence

<400> 33  
atggttggtgta ctactactct gaacactggt gcatctctgg aactggtagg ttatggtact 60  
tggcaagctg ctccgggcga agtaggtcaa ggtgtaaaag tagctatcga aactggttat 120  
cgtcatctgg atctggcaaa agtatactct aaccagccgg aagtaggtgc agcaatcaag 180  
gaagctggcg ttaaactgga ggatctgttt atcacttcta aactgtggaa caactccac 240  
cgtccggaac aggtagaacc ggctctggat gatactctga aagaactggg cctggagtat 300  
ctggacctgt acctgatcca ctggccggtg gcatctccgc cggaaggtga tatcactcag 360  
aacctgttcc cgaaagctaa cgataaagaa gtaaaactgg acctggaagt ttctctggta 420  
gacacttgga aagcaatggt aaaactgctg gatactggta aagttaaagc tatcgggtgtt 480  
tccaactttg acgcaaaaat ggttgacgct atcatcgaag caactggcgt aactccgtct 540  
gttaaccaga tcgaacgtca cccgctgctg ctgcagccag agctgatcgc acaccacaaa 600  
gctaaaaaca tccacatcac cgcatactcc ccgctgggta acaacaccgt aggcgcaccg 660



15

Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp  
 325 330 335

Leu Val Gly Ser Glu Thr Ala  
 340

<210> 36  
 <211> 1032  
 <212> DNA  
 <213> Artificial Sequence

<400> 36  
 atggctaaaa tcgataacgc agttctgccg gaaggttccc tggttctggt tacgggtgct 60  
 aacgggtttcg ttggttccca cgttggtgaa cagctgctgg aacacggtta caaagttcgt 120  
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttgga cgctaaatac 180  
 ccgggtcggt tcgaaaccgc tgttggtgaa gacatgctga aacaggtgc ttacgacgaa 240  
 gttatcaaag gtgctgctgg tgttgctcac atcgcttccg ttgtttcctt ctccaacaaa 300  
 tacgacgaag ttgttacccc ggctatcggt ggtaccctga acgctctgcg tgctgctgct 360  
 gctaccccggt ccgttaaacy tttcgttctg acctcctcca ccgtttccgc totgatcccg 420  
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatogac 480  
 aaagctaaaa cctgcccga atccgacccg cagaaatccc tgtgggtata cgctgcatcc 540  
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc aactttcact 600  
 ctgaacgctg tactgcaaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660  
 ggttccacct ccggttggt gatgtccctg tttaacggcg aggtttcccc ggctctggct 720  
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggtgc 780  
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta ctgctggtac tttcgattgg 840  
 aacaccgttc tggctacctt ccgtaaactg taccgctcca aaaccttccc ggctgacttc 900  
 ccagatcaag gtcaggacct gtctaaatto gacaccgctc cgtccctgga aattctgaaa 960  
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020  
 gaaaccgctt aa 1032

<210> 37  
 <211> 343  
 <212> PRT  
 <213> Artificial Sequence

<400> 37

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu  
 1 5 10 15

Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu

	20						25						30					
Leu	Glu	His 35	Gly	Tyr	Lys	Val	Arg 40	Gly	Thr	Ala	Arg	Ser 45	Ala	Ser	Lys			
Leu	Ala 50	Asn	Leu	Gln	Lys	Arg 55	Trp	Asp	Ala	Lys	Tyr 60	Pro	Gly	Arg	Phe			
Glu 65	Thr	Ala	Val	Val 70	Glu	Asp	Met	Leu	Lys	Gln 75	Gly	Ala	Tyr	Asp	Glu 80			
Val	Ile	Lys	Gly	Ala 85	Ala	Gly	Val	Ala	His 90	Ile	Ala	Ser	Val	Val 95	Ser			
Phe	Ser	Asn	Lys 100	Tyr	Asp	Glu	Val	Val 105	Thr	Pro	Ala	Ile	Gly 110	Gly	Thr			
Leu	Asn	Ala 115	Leu	Arg	Ala	Ala	Ala 120	Ala	Thr	Pro	Ser	Val 125	Lys	Arg	Phe			
Val	Leu 130	Thr	Ser	Ser	Thr	Val 135	Ser	Ala	Leu	Ile	Pro 140	Lys	Pro	Asn	Val			
Glu 145	Gly	Ile	Tyr	Leu	Asp 150	Glu	Lys	Ser	Trp	Asn 155	Leu	Glu	Ser	Ile	Asp 160			
Lys	Ala	Lys	Thr	Leu 165	Pro	Glu	Ser	Asp	Pro 170	Gln	Lys	Ser	Leu	Trp 175	Val			
Tyr	Ala	Ala	Ser 180	Lys	Thr	Glu	Ala	Glu 185	Leu	Ala	Ala	Trp	Lys 190	Phe	Met			
Asp	Glu	Asn 195	Lys	Pro	His	Phe	Thr 200	Leu	Asn	Ala	Val	Leu 205	Pro	Asn	Tyr			
Thr	Ile 210	Gly	Thr	Ile	Phe	Asp 215	Pro	Glu	Thr	Gln	Ser 220	Gly	Ser	Thr	Ser			
Gly 225	Trp	Met	Met	Ser	Leu 230	Phe	Asn	Gly	Glu	Val 235	Ser	Pro	Ala	Leu	Ala 240			
Leu	Met	Pro	Pro	Gln 245	Tyr	Tyr	Val	Ser	Ala 250	Val	Asp	Ile	Gly	Leu 255	Leu			
His	Leu	Gly	Cys 260	Leu	Val	Leu	Pro	Gln 265	Ile	Glu	Arg	Arg 270	Arg	Val	Tyr			
Gly	Thr	Ala 275	Gly	Thr	Phe	Asp	Trp 280	Asn	Thr	Val	Leu	Ala 285	Thr	Phe	Arg			
Lys	Leu 290	Tyr	Pro	Ser	Lys	Thr 295	Phe	Pro	Ala	Asp	Phe 300	Pro	Asp	Gln	Gly			
Gln 305	Asp	Leu	Ser	Lys	Phe 310	Asp	Thr	Ala	Pro	Ser 315	Leu	Glu	Ile	Leu	Lys 320			
Ser	Leu	Gly	Arg	Pro 325	Gly	Trp	Arg	Ser	Ile 330	Glu	Glu	Ser	Ile	Lys 335	Asp			
Leu	Val	Gly	Ser 340	Glu	Thr	Ala												

<210> 38  
 <211> 942  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*  
  
 <400> 38  
 atgggtcctg ctacgttaaa gaattcttct gctacattaa aactaaatac tgggtgcctcc 60  
 attccagtgt tgggtttcgg cacttggcgt tccgttgaca ataacggtta ccattctgta 120  
 attgcagctt tgaaagctgg atacagacac attgatgctg cggctatcta tttgaatgaa 180  
 gaagaagttg gcagggctat taaagattcc ggagtccctc gtgaggaaat ttttattact 240  
 actaagcttt ggggtacgga acaacgtgat ccggaagctg ctctaaacaa gtctttgaaa 300  
 agactaggct tggattatgt tgacctatat ctgatgcatt ggccagtgcc tttgaaaacc 360  
 gacagagtta ctgatggtaa cgttctgtgc attccaacat tagaagatgg cactgttgac 420  
 atcgatacta aggaatggaa ttttatcaag acgtgggagt tgatgcaaga gttgccaaag 480  
 acgggcaaaa ctaaagccgt tgggtgtctct aatttttcta ttaacaacat taaagaatta 540  
 ttagaatctc caaataacaa ggtggtacca gctactaatc aaattgaaat tcatccattg 600  
 ctaccacaag acgaattgat tgccttttgt aaggaaaagg gtattgttgt tgaagcctac 660  
 tcaccatttg ggagtgctaa tgctccttta ctaaagagc aagcaattat tgatatggct 720  
 aaaaagcacg gcgttgagcc agcacagctt attatcagtt ggagtattca aagaggctac 780  
 gttgttctgg ccaaatcggg taatcctgaa agaattgtat ccaattttaa gattttcact 840  
 ctgcctgagg atgatttcaa gactattagt aacctatcca aagtgcattg tacaaagaga 900  
 gtcgttgata tgaagtgggg atccttccca attttccaat ga 942

<210> 39  
 <211> 313  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 39  
 Met Gly Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn  
 1 5 10 15  
 Thr Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val  
 20 25 30  
 Asp Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr  
 35 40 45  
 Arg His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly  
 50 55 60  
 Arg Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr  
 65 70 75 80

Thr Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn  
85 90 95

Lys Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met  
100 105 110

His Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val  
115 120 125

Leu Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys  
130 135 140

Glu Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys  
145 150 155 160

Thr Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn  
165 170 175

Ile Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr  
180 185 190

Asn Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala  
195 200 205

Phe Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly  
210 215 220

Ser Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala  
225 230 235 240

Lys Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile  
245 250 255

Gln Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile  
260 265 270

Val Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr  
275 280 285

Ile Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met  
290 295 300

Lys Trp Gly Ser Phe Pro Ile Phe Gln  
305 310

<210> 40  
<211> 942  
<212> DNA  
<213> Artificial Sequence

<400> 40  
atgggtccgg caactctgaa gaactcttct gcaactctga aactgaacac tgggtgcatct 60  
atcccggttc tgggtttcgg tacttggcgt tctgttgaca acaacgggta ccaactccggt 120  
atcgacgac tgaaagcagg ttaccgtcac atcgacgcag cagcaatcta cctgaacgaa 180  
gaagaagtag gtcgtgcaat caaagactcc ggtgttccgc gtgaagaaat ctttatcact 240  
actaaactgt ggggtactga acagcgtgac ccggaagcag cactgaacaa atctctgaaa 300





<210> 42  
 <211> 312  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 42

Met	Pro	Ala	Thr	Leu	His	Asp	Ser	Thr	Lys	Ile	Leu	Ser	Leu	Asn	Thr
1				5					10					15	
Gly	Ala	Gln	Ile	Pro	Gln	Ile	Gly	Leu	Gly	Thr	Trp	Gln	Ser	Lys	Glu
			20					25					30		
Asn	Asp	Ala	Tyr	Lys	Ala	Val	Leu	Thr	Ala	Leu	Lys	Asp	Gly	Tyr	Arg
		35					40					45			
His	Ile	Asp	Thr	Ala	Ala	Ile	Tyr	Arg	Asn	Glu	Asp	Gln	Val	Gly	Gln
	50					55					60				
Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Val	Thr	Thr
65					70					75					80
Lys	Leu	Trp	Cys	Thr	Gln	His	His	Glu	Pro	Glu	Val	Ala	Leu	Asp	Gln
			85					90						95	
Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Met	His
			100					105					110		
Trp	Pro	Ala	Arg	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Asn	Glu	Asp	Ile	Leu
		115					120					125			
Ser	Val	Pro	Thr	Lys	Lys	Asp	Gly	Ser	Arg	Ala	Val	Asp	Ile	Thr	Asn
	130					135					140				
Trp	Asn	Phe	Ile	Lys	Thr	Trp	Glu	Leu	Met	Gln	Glu	Leu	Pro	Lys	Thr
145					150					155				160	
Gly	Lys	Thr	Lys	Ala	Val	Gly	Val	Ser	Asn	Phe	Ser	Ile	Asn	Asn	Leu
				165					170					175	
Lys	Asp	Leu	Leu	Ala	Ser	Gln	Gly	Asn	Lys	Leu	Thr	Pro	Ala	Ala	Asn
		180						185					190		
Gln	Val	Glu	Ile	His	Pro	Leu	Leu	Pro	Gln	Asp	Glu	Leu	Ile	Asn	Phe
	195						200					205			
Cys	Lys	Ser	Lys	Gly	Ile	Val	Val	Glu	Ala	Tyr	Ser	Pro	Leu	Gly	Ser
	210					215					220				
Thr	Asp	Ala	Pro	Leu	Leu	Lys	Glu	Pro	Val	Ile	Leu	Glu	Ile	Ala	Lys
225					230					235					240
Lys	Asn	Asn	Val	Gln	Pro	Gly	His	Val	Val	Ile	Ser	Trp	His	Val	Gln
			245						250					255	
Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Val	Asn	Pro	Asp	Arg	Ile	Lys
			260					265					270		
Thr	Asn	Arg	Lys	Ile	Phe	Thr	Leu	Ser	Thr	Glu	Asp	Phe	Glu	Ala	Ile

285

Glu Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr

[illegible]

<400> 45  
atgtcagttt tggtttcagg tgctaacggg ttcattgcc aacacattgt cgatctcctg

23

ttgaaggaag	actataaggt	catcggttct	gccagaagtc	aagaaaaggc	cgagaattta	120
acggaggcct	ttggtaacaa	cccaaaattc	tocatggaag	ttgtcccaga	catatctaag	180
ctggacgcat	ttgaccatgt	tttccaaaag	cacggcaagg	atatcaagat	agttctacat	240
acggcctctc	cattctgctt	tgatatcact	gacagtgaac	gcgattttatt	aattcctgct	300
gtgaacggtg	ttaagggaat	tctccactca	attaaaaaat	acgccgctga	ttctgtagaa	360
cgtgtagttc	tcacctcttc	ttatgcagct	gtgttcgata	tggcaaaaga	aaacgataag	420
tctttaacat	ttaacgaaga	atcctggaac	ccagctacct	gggagagttg	ccaaagtgac	480
ccagttaacg	cctactgtgg	ttctaagaag	tttgctgaaa	aagcagcttg	ggaattttcta	540
gaggagaata	gagactctgt	aaaattcgaa	ttaactgcog	ttaaccagct	ttacgttttt	600
ggtccgcaaa	tgtttgacaa	agatgtgaaa	aaacacattga	acacatcttg	cgaactcgtc	660
aacagcttga	tgcatttatc	accagaggac	aagataccgg	aactatttgg	tggatacatt	720
gatgttcgtg	atgttgcaaa	ggctcattta	gttgccttcc	aaaagaggga	aacaattgggt	780
caaagactaa	tcgtatcgga	ggccagattt	actatgcagg	atgtttctcga	tatccttaac	840
gaagacttcc	ctgttctaaa	aggcaatatt	ccagtgggga	aaccaggttc	tggtgctacc	900
cataacaccc	ttggtgctac	tcttgataat	aaaaagagta	agaaattggt	aggtttcaag	960
ttcaggaact	tgaaagagac	cattgacgac	actgcctccc	aaattttaaa	atttgagggc	1020
agaatataa						1029

```
<210> 46
<211> 342
<212> PRT
<213> Saccharomyces cerevisiae

<400> 46
```

Met Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His Ile  
1 5 10 15

Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala Arg  
20 25 30

Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn Pro  
35 40 45

Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala Phe  
50 55 60

Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu His  
65 70 75 80

Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp Leu  
85 90 95

Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile Lys

[illegible]

```
<210> 47
<211> 1032
<212> DNA
<213> Artificial Sequence
```

```
<400> 47
atgggctctg tatttgatc tggcgctaac ggttttatcg ctcaacacat cgtcgatctg 60
ctgctgaaaag aagattacaa agttatcggg tccgcacggt ccaggaaaa agctgaaaac 120
ctgactgaag catttggtaa caaccgaag ttctctatgg aagtagtacc ggacatttct 180
aaactggacg cattcgacca cgtattccaa aagcacggta aggatatcaa gatcgactg 240
```









Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu  
 180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe  
 195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro  
 210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr  
 225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
 245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
 260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
 275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
 290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
 305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala  
 325

<210> 51  
 <211> 987  
 <212> DNA  
 <213> Artificial Sequence

<400> 51  
 atgggctctt ctctggtaac tctgaacaac ggtctgaaaa tgccgctggt aggcctgggc 60  
 tgctggaaaa tcgataagaa agtatgtgct aaccaaattt atgaggctat caaactgggc 120  
 tatcgctgtg tcgacggtgc ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180  
 cgtaaagcta tctctgaagg tctggtatct cgtaaggata tctttgtagt atctaagctg 240  
 tggaacaact ttcataccccc ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300  
 atgggtctgg attatctgga tctgtactat atccactttc cgatcgcat taaatacgtg 360  
 cggttcgaag aaaaatatcc gccgggcttt tacactgggtg cagacgacga aaagaagggt 420  
 cacatcactg aagctcacgt accgatcatc gacacttacc gtgctctgga ggaatgtgta 480  
 gacgaaggtc tgatcaaata tatcggtgta tctaacttcc agggttctct gatccaggat 540  
 ctgctgcgtg gttgccgtat caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600  
 acccaggaac acctgggttg attctgcaaa ctgcacgata tccaagtagt agcatactct 660  
 tctttcggtc cgcagtcctt catcgaaatg gacctgcagc tggctaagac caccgccact 720  
 ctgttcgaaa acgacgtaat caagaaagta tctcagaacc acccgggctc tactacctct 780



Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
 245 250 255  
 Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
 260 265 270  
 Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
 275 280 285  
 Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
 290 295 300  
 Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
 305 310 315 320  
 Asp Gly Lys Phe Pro Thr Phe Ala  
 325

<210> 53  
 <211> 1461  
 <212> DNA  
 <213> Sus scrofa

<400> 53  
 atgaatgcca gcgatttcgc tcgacgcggc aaagaaatgg tggattacat ggcggtattac 60  
 ctggaaggca tcgaaggctc tcaggtgtac ccgcatgtgc agccggggta cctgcgtccg 120  
 ctgatcccg cgaccgcccc gcaggaaccg gataccttcg aagatattct gcaggatgtg 180  
 gaaaaaatca tcatgccggg ggtgaccac tggcacagcc cgtacttctt cgcgtacttc 240  
 ccgaccgcca gcagctaccc ggcgatgctg gcggatatgc tgtgcggtgc gatcggtatgc 300  
 atcggtttca gctgggcggc tagccggcg tgcaccgaac tcgagaccgt gatgatggat 360  
 tggctgggca aaatgctcca gcttcggaa gcgttcctgg cgggcgaagc cgggtgaaggc 420  
 ggcggcgtga tccagggtag cgcagcgaa gccaccctgg tggcgctgct ggcggcgctg 480  
 accaaagtgg tgcgacgtct gcaagcggcg agccggggcc tgaccaggg cgcggtgctg 540  
 gaaaaactag tggcgtagc gagtgatcag gcgcacagca gcgtggaac tgccggcctg 600  
 atcgggggcg tgaaactgaa agcgatcccg agcgatggca aattcgcat gcgtgcgagc 660  
 gcgctgcagg aggccttga gagagacaag gctgccggcc tgattcctt ctctgtggtg 720  
 gctacgtctg ggaccacatc gtgctgctcc ttgacaatc tcttagaagt gggaccatc 780  
 tgtcacgaag aggacatatg gctgcacgtg gatgctgcct acgcaggcag tgccttcac 840  
 tgccctgagt tccggcacct gctgaatgga gtggagtttg cagattcatt taactttaat 900  
 cccacaaat ggctcttggg gaattttgac tgctcggtc tgtgggtgaa aaggagaacg 960  
 gacctgactg gagccttcaa attggacccc gtgtacttaa agcacagcca ccagggtctg 1020  
 gggcttatca cggactacag gcaactggc ctgccactgg gtcggcgatt ccggtccctg 1080



[illegible]

```
<210> 55
<211> 1464
<212> DNA
<213> Artificial Sequence
```

<400> 55  
atgggctaacg cttccgattt ccgtcgtcgt ggcaaagaaa tggtagacta catggcagat

60

tatctggaag gtatcgaagg ccgtcaagtt taccoggacg ttcagccagg ctatctgcgt	120
ccgctcatcc cagctaccgc accgcaagaa ccggacacct ttgaagacat cctgcaagac	180
gtagaaaaga tcatcatgcc aggtgtaacc cactggcaact ctccgtactt tttcgcatatc	240
ttcccgactg catcctccta cccggctatg ctggctgaca tgctgtgtgg tgctatcggc	300
tgtatcggct tttcctgggc tgcattctccg gcattgcaact agctggaaac cgttatgatg	360
gattggctgg gtaaaatgct gcagctgcca gaggcatttc tggctgggtga ggctgggtgag	420
gggtgggtgg taattcaagg ctctgcgtcc gaagctactc tgggtgctct gctggctgct	480
cgtactaaag ttgttcgtcg tctgcaagct gcattctccg gtctgactca ggggtgctgtt	540
ctggagaaaac tggtagcgta tgcttctgat caggctcaact ctcccggtga gcgtgctggt	600
ctgattgggtg gtgttaagct gaaagctatt ccgtccgatg gtaagtccgc tatgcgtgca	660
tccgctctgc aagaagctct ggaacgtgac aaagctgctg gtctgattcc gttcttcggt	720
gttgctaccc tgggtactac ctcttgctgt tctttcgaca acctgctgga agttgggtccg	780
atctgtcacg aggaggacat ctggctgcac gttgacgcag catatgctgg ctctgctttt	840
atctgtccgg aattccgtca cctgctgaac ggcgttgagt tcgctgattc tttcaacttc	900
aaccgcaca agtggctgct ggttaacttt gattgctcgg ctatgtgggt aaaacgtcgc	960
actgatctga ccggtgcatt taaactggac ccggtatata tgaagcattc tcaccagggt	1020
tccggcctga ttaccgatta tcgtcattgg cagctgccgc tgggtcgtcg ttttcgttcg	1080
ctgaagatgt ggttcgtatt ccgtatgtac ggcgttaaag gtctgcaagc atacatccgt	1140
aaacacgttc aactgtcgca cgagttcgaa gctttcgtac tgcaggacct gcgttttgaa	1200
gtttgcgctg aagttaccct gggcctgggt tgcttcgcgc tgaagggttc tgatggctg	1260
aacgaagctc tgctggagcg tattaactcg gctcgtaaaa tccacctggt tccgtgctg	1320
ctgcgtggtc agttcgttct gcgcttcgct atttgttcgc gtaaggtaga gtctggcat	1380
gttcgtctgg catgggagca catccgtggt ctggctgctg aactgctggc tgctgaagaa	1440
ggtaaggctg aaatcaaata ctaa	1464

<210> 56  
 <211> 487  
 <212> PRT  
 <213> Artificial Sequence

<400> 56

Met	Gly	Asn	Ala	Ser	Asp	Phe	Arg	Arg	Arg	Gly	Lys	Glu	Met	Val	Asp
1				5					10					15	

Tyr	Met	Ala	Asp	Tyr	Leu	Glu	Gly	Ile	Glu	Gly	Arg	Gln	Val	Tyr	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20				25				30							
Asp	Val	Gln	Pro	Gly	Tyr	Leu	Arg	Pro	Leu	Ile	Pro	Ala	Thr	Ala	Pro
		35					40					45			
Gln	Glu	Pro	Asp	Thr	Phe	Glu	Asp	Ile	Leu	Gln	Asp	Val	Glu	Lys	Ile
	50					55					60				
Ile	Met	Pro	Gly	Val	Thr	His	Trp	His	Ser	Pro	Tyr	Phe	Phe	Ala	Tyr
65					70					75					80
Phe	Pro	Thr	Ala	Ser	Ser	Tyr	Pro	Ala	Met	Leu	Ala	Asp	Met	Leu	Cys
				85					90					95	
Gly	Ala	Ile	Gly	Cys	Ile	Gly	Phe	Ser	Trp	Ala	Ala	Ser	Pro	Ala	Cys
			100					105					110		
Thr	Glu	Leu	Glu	Thr	Val	Met	Met	Asp	Trp	Leu	Gly	Lys	Met	Leu	Gln
		115					120					125			
Leu	Pro	Glu	Ala	Phe	Leu	Ala	Gly	Glu	Ala	Gly	Glu	Gly	Gly	Gly	Val
	130					135					140				
Ile	Gln	Gly	Ser	Ala	Ser	Glu	Ala	Thr	Leu	Val	Ala	Leu	Leu	Ala	Ala
145					150					155					160
Arg	Thr	Lys	Val	Val	Arg	Arg	Leu	Gln	Ala	Ala	Ser	Pro	Gly	Leu	Thr
				165					170					175	
Gln	Gly	Ala	Val	Leu	Glu	Lys	Leu	Val	Ala	Tyr	Ala	Ser	Asp	Gln	Ala
			180					185					190		
His	Ser	Ser	Val	Glu	Arg	Ala	Gly	Leu	Ile	Gly	Gly	Val	Lys	Leu	Lys
		195					200					205			
Ala	Ile	Pro	Ser	Asp	Gly	Lys	Phe	Ala	Met	Arg	Ala	Ser	Ala	Leu	Gln
	210					215					220				
Glu	Ala	Leu	Glu	Arg	Asp	Lys	Ala	Ala	Gly	Leu	Ile	Pro	Phe	Phe	Val
225					230					235					240
Val	Ala	Thr	Leu	Gly	Thr	Thr	Ser	Cys	Cys	Ser	Phe	Asp	Asn	Leu	Leu
				245					250					255	
Glu	Val	Gly	Pro	Ile	Cys	His	Glu	Glu	Asp	Ile	Trp	Leu	His	Val	Asp
			260					265					270		
Ala	Ala	Tyr	Ala	Gly	Ser	Ala	Phe	Ile	Cys	Pro	Glu	Phe	Arg	His	Leu
		275					280					285			
Leu	Asn	Gly	Val	Glu	Phe	Ala	Asp	Ser	Phe	Asn	Phe	Asn	Pro	His	Lys
	290					295					300				
Trp	Leu	Leu	Val	Asn	Phe	Asp	Cys	Ser	Ala	Met	Trp	Val	Lys	Arg	Arg
305				310						315					320
Thr	Asp	Leu	Thr	Gly	Ala	Phe	Lys	Leu	Asp	Pro	Val	Tyr	Leu	Lys	His
				325					330					335	
Ser	His	Gln	Gly	Ser	Gly	Leu	Ile	Thr	Asp	Tyr	Arg	His	Trp	Gln	Leu
			340					345					350		

Pro Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg  
 355 360 365  
 Met Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln  
 370 375 380  
 Leu Ser His Glu Phe Glu Ala Phe Val Leu Gln Asp Pro Arg Phe Glu  
 385 390 395 400  
 Val Cys Ala Glu Val Thr Leu Gly Leu Val Cys Phe Arg Leu Lys Gly  
 405 410 415  
 Ser Asp Gly Leu Asn Glu Ala Leu Leu Glu Arg Ile Asn Ser Ala Arg  
 420 425 430  
 Lys Ile His Leu Val Pro Cys Arg Leu Arg Gly Gln Phe Val Leu Arg  
 435 440 445  
 Phe Ala Ile Cys Ser Arg Lys Val Glu Ser Gly His Val Arg Leu Ala  
 450 455 460  
 Trp Glu His Ile Arg Gly Leu Ala Ala Glu Leu Leu Ala Ala Glu Glu  
 465 470 475 480  
 Gly Lys Ala Glu Ile Lys Ser  
 485

<210> 57  
 <211> 1098  
 <212> DNA  
 <213> Candida boidinii

<400> 57  
 atgggtaaga ttgtcttagt tctttatgat gctggtaagc acgctgctga tgaagaaaaa 60  
 ttatatggtt gtactgaaaa taaattaggt attgctaatt ggtaaaaaga tcaaggatcat 120  
 gaactaatta ctacttctga taaagaaggt gaaacaagtg aattggataa acatatccca 180  
 gatgctgata ttatcatcac cactcctttc catcctgctt atatcactaa ggaaagactt 240  
 gacaaggcta agaacttaaa attagtcgtt gtcgctgggtg ttggttctga tcacattgat 300  
 ttagattata ttaatcaaac aggtaagaaa atctcagtcg tggaagttac aggtttcta 360  
 gttgtctctg ttgctgaaca cgttgctcatg accatgcttg tcttggttag aaatttcggt 420  
 ccagcacatg aacaaattat taaccacgat tgggagggtg ctgctatcgc taaggatgct 480  
 tacgatatcg aaggtaaaac tatcgtacc attggtgctg gtagaattgg ttacagagtc 540  
 ttggaaagat tactcccatt taatccaaaa gaattattat actacgatta tcaagcttta 600  
 ccaaaagaag ctgaagaaaa agttggtgct agaagagttg aaaatattga agaattagtt 660  
 gctcaagctg atatcggttac agttaatgct ccattacacg caggtaaaaa aggtttaatt 720  
 aataaggaat tattatctaa atttaaaaaa ggtgcttggt tagtcaatac cgcaagaggt 780  
 gctatttggtg ttgctgaaga tgttgcagca gctttagaat ctggtcaatt aagaggttac 840



ggtggtgatg tttggttccc acaaccagct ccaaaggatc acccatggag agatatgaga 900  
aataaatatg gtgctggtaa tgccatgact cctcactact ctggtactac tttagacgct 960  
caaacaagat acgctgaagg tactaaaaat attttggaaat cattctttac cggtaaattt 1020  
gattacagac cacaagatat tatcttatta aatggtgaat acgttactaa agcttacggt 1080  
aaacacgata agaaataa 1098

<210> 58  
<211> 365  
<212> PRT  
<213> Candida boidinii

<400> 58

Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala  
1 5 10 15  
Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala  
20 25 30  
Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys  
35 40 45  
Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile  
50 55 60  
Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu  
65 70 75 80  
Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser  
85 90 95  
Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser  
100 105 110  
Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val  
115 120 125  
Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu  
130 135 140  
Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala  
145 150 155 160  
Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile  
165 170 175  
Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu  
180 185 190  
Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val  
195 200 205  
Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp  
210 215 220



ggtggtgacg tatggtttcc gcagccggct ccgaaagatc acccgtggcg tgatatgcgt 900  
 aacaaatatg gcgctggtaa cgcaatgacc ccgcactact ctggtaccac tctggatgct 960  
 cagacccggt acgctgaagg tactaaaaac atcctggaat ctttcttcac tggtaaattc 1020  
 gactaccgcc cgcaggacat cattctgctg aacgggtgaat atgtaactaa agcttacggc 1080  
 aaacacgaca aaaaataa 1098

<210> 60  
 <211> 365  
 <212> PRT  
 <213> Artificial Sequence

<400> 60

Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala  
 1 5 10 15  
 Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala  
 20 25 30  
 Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys  
 35 40 45  
 Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile  
 50 55 60  
 Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu  
 65 70 75 80  
 Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser  
 85 90 95  
 Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser  
 100 105 110  
 Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val  
 115 120 125  
 Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu  
 130 135 140  
 Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala  
 145 150 155 160  
 Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile  
 165 170 175  
 Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu  
 180 185 190  
 Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val  
 195 200 205  
 Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp  
 210 215 220  
 Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.45	0.50	0	1
Marital status	0.65	0.48	0	1
Education	12.5	1.5	9	16
Income	15.2	8.5	5	35
Health status	0.75	0.42	0	1
Employment	0.85	0.35	0	1
Stress level	4.2	1.8	1	7
Life satisfaction	5.8	1.2	3	7
Depression	0.35	0.48	0	1
Loneliness	0.45	0.52	0	1
Self-esteem	4.5	1.5	1	7
Resilience	5.2	1.8	1	7
Optimism	5.5	1.5	1	7
Gratitude	5.8	1.2	1	7
Forgiveness	5.5	1.5	1	7
Compassion	5.2	1.8	1	7
Empathy	5.5	1.5	1	7
Kindness	5.8	1.2	1	7
Generosity	5.5	1.5	1	7
Patience	5.2	1.8	1	7
Humility	5.5	1.5	1	7
Modesty	5.8	1.2	1	7
Shame	0.35	0.48	0	1
Guilt	0.45	0.52	0	1
Envy	0.35	0.48	0	1
Jealousy	0.45	0.52	0	1
Anger	0.35	0.48	0	1
Dislike	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1
Disobedience	0.45	0.52	0	1
Disloyalty	0.35	0.48	0	1
Disaffection	0.45	0.52	0	1
Disrespect	0.35	0.48	0	1</

40







<400> 64

Met	Gly	Ser	Leu	Leu	Ile	Arg	Gly	Ala	Thr	Val	Val	Thr	His	Glu	Glu	
1			5						10					15		
Ser	Tyr	Pro	Ala	Asp	Val	Leu	Cys	Val	Asp	Gly	Leu	Ile	Arg	Ala	Ile	
			20					25					30			
Gly	Pro	Asn	Leu	Glu	Pro	Pro	Thr	Asp	Cys	Glu	Ile	Leu	Asp	Gly	Ser	
		35					40					45				
Gly	Gln	Tyr	Leu	Met	Pro	Gly	Gly	Ile	Asp	Pro	His	Thr	His	Met	Gln	
	50					55					60					
Leu	Pro	Phe	Met	Gly	Thr	Val	Ala	Ser	Glu	Asp	Phe	Phe	Ser	Gly	Thr	
65					70					75					80	
Ala	Ala	Gly	Leu	Ala	Gly	Gly	Thr	Thr	Ser	Ile	Ile	Asp	Phe	Val	Ile	
			85						90					95		
Pro	Asn	Pro	Gln	Gln	Ser	Leu	Leu	Glu	Ala	Phe	His	Thr	Trp	Arg	Gly	
			100					105						110		
Trp	Ala	Gln	Lys	Ser	Ala	Ser	Asp	Tyr	Gly	Phe	His	Val	Ala	Ile	Thr	
		115					120					125				
Trp	Trp	Ser	Glu	Gln	Val	Ala	Glu	Glu	Met	Gly	Glu	Leu	Val	Ala	Lys	
	130					135					140					
His	Gly	Val	Asn	Ser	Phe	Lys	His	Phe	Met	Ala	Tyr	Lys	Asn	Ala	Ile	
145					150					155					160	
Met	Ala	Ala	Asp	Asp	Thr	Leu	Val	Ala	Ser	Phe	Glu	Arg	Cys	Leu	Gln	
			165						170					175		
Leu	Gly	Ala	Val	Pro	Thr	Val	His	Ala	Glu	Asn	Gly	Glu	Leu	Val	Tyr	
		180						185					190			
His	Leu	Gln	Lys	Lys	Leu	Leu	Ala	Gln	Gly	Met	Thr	Gly	Pro	Glu	Ala	
	195						200					205				
His	Pro	Leu	Ser	Arg	Pro	Ser	Gln	Val	Glu	Gly	Glu	Ala	Ala	Ser	Arg	
	210					215					220					
Ala	Ile	Arg	Ile	Ala	Glu	Thr	Ile	Gly	Thr	Pro	Leu	Tyr	Val	Val	His	
225					230					235					240	
Ile	Ser	Ser	Arg	Glu	Ala	Leu	Asp	Glu	Ile	Thr	Tyr	Ala	Arg	Ala	Lys	
			245					250						255		
Gly	Gln	Pro	Val	Tyr	Gly	Glu	Val	Leu	Pro	Gly	His	Leu	Leu	Leu	Asp	
			260					265					270			
Asp	Ser	Val	Tyr	Arg	Asp	Pro	Asp	Trp	Ala	Thr	Ala	Ala	Gly	Tyr	Val	
		275					280					285				
Met	Ser	Pro	Pro	Phe	Arg	Pro	Arg	Glu	His	Gln	Glu	Ala	Leu	Trp	Arg	
	290					295					300					
Gly	Leu	Gln	Ser	Gly	Asn	Leu	His	Thr	Thr	Ala	Thr	Asp	His	Cys	Cys	





```

gaagtcgtcc ttgcgaatgg cgagcttctt aggactggca tgggggctct acctgaccc 660
aaacgtcccg aaacgatggg gctaaagcca gaagaccagc catggagcaa aatcgctcat 720
ctgtttcctt atggcttcgg tcctatatata gatgggctat tcagccaatc gaatatggga 780
attgttacca agatcgggat ctgggtaatg cccaatccag ggggttatca atcctacttg 840
atcacactac ccaaagatgg tgatttaaaa caagccgtcg atattattcg tccccttcgt 900
ctaggcatgg cccttcaaaa tgttcccact attogccaca ttcttttgga tgcagcggtg 960
ctcggtgaca agcgatctta ttcattccaag accgaacccc tctccgacga ggaattagac 1020
aagatcgcca aacagctcaa cttgggacga tggaactttt acggggcgct ctatggacct 1080
gagccgattc gaagggttct ctgggaaacg attaaagacg cattctcggc gatcccaggc 1140
gtcaagtttt attttcggga ggacactcct gaaaactccg ttctccgcgt gcgtgataag 1200
actatgcaag gcattccaac ttacgacgag cttaaagtga tcgattggct ccctaattgt 1260
gcgcatctgt tcttctctcc tattgcgaag gtatctggtg aagatgcaat gatgcaatac 1320
gcagtcacca agaaaagggtg tcaggaggct ggggttagatt ttatcggcac ttccacagtc 1380
ggtatgagag agatgcatca tatcgtttgt attgtgttca acaagaagga cctaatacaa 1440
aagagaaaag tacagtggct gatgagaacc cttattgatg actgtgctgc aaatggatgg 1500
ggcgaatatc gaacccatct ggccttcattg gaccaaatta tggaaacctt caactggaac 1560
aacagcagct tctaagggtt caatgaggtc ctcaagaatg cggtggatcc taatggcatc 1620
attgcccccg gaaagtctgg tgtttggccg agtcaatata gtcattgttac ttggaaactg 1680
taa 1683

```

```

<210> 66
<211> 560
<212> PRT
<213> Penicillium simplicissimum

```

<400> 66

```

Met Ser Lys Thr Gln Glu Phe Arg Pro Leu Thr Leu Pro Pro Lys Leu
1          5          10          15
Ser Leu Ser Asp Phe Asn Glu Phe Ile Gln Asp Ile Ile Arg Ile Val
20        25        30
Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val Asp
35        40        45
Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val Met
50        55        60
Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn Val
65        70        75        80

```



405	410	415
Leu Pro Asn Gly Ala His Leu Phe Phe Ser Pro Ile Ala Lys Val Ser		
420	425	430
Gly Glu Asp Ala Met Met Gln Tyr Ala Val Thr Lys Lys Arg Cys Gln		
435	440	445
Glu Ala Gly Leu Asp Phe Ile Gly Thr Phe Thr Val Gly Met Arg Glu		
450	455	460
Met His His Ile Val Cys Ile Val Phe Asn Lys Lys Asp Leu Ile Gln		
465	470	475
Lys Arg Lys Val Gln Trp Leu Met Arg Thr Leu Ile Asp Asp Cys Ala		
485	490	495
Ala Asn Gly Trp Gly Glu Tyr Arg Thr His Leu Ala Phe Met Asp Gln		
500	505	510
Ile Met Glu Thr Tyr Asn Trp Asn Asn Ser Ser Phe Leu Arg Phe Asn		
515	520	525
Glu Val Leu Lys Asn Ala Val Asp Pro Asn Gly Ile Ile Ala Pro Gly		
530	535	540
Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys Leu		
545	550	555
560		

<210> 67  
 <211> 1686  
 <212> DNA  
 <213> Artificial Sequence

<400> 67	
atgggctcta aaactcagga gttccgtccg ctgaccctgc cgccgaaact gtctctgtct	60
gattttaacg aattcatcca ggatatcatc cgtatcggtg gttctgaaaa cgttgaagtt	120
atctcttcta aagaccagat cgttgacggt tcttacatga aaccgaccca caccacgac	180
ccgcaccacg ttatggacca ggactacttc ctggcttctg ctatcgttgc tccgcgtaac	240
gttgctgacg ttcagtctat cgttggtctg gctaacaaat tctctttccc gctgtggcog	300
atctctatcg gtcgtaactc tggttacggt ggtgctgctc cgcgtgttcc tggttctggt	360
gttctggaca tgggtaaaaa catgaaccgt gttctggaag ttaacgttga aggtgcttac	420
tgcgttggtg aaccgggtgt aacttatcat gacctgcaca actacctgga agctaacaac	480
ctgcgtgaca aactgtggct ggacgtaccg gatctgggtg gtggttctgt tctgggtaac	540
gctgttgaaac gtggtgttgg ttacaccccg tacggtgatc attggatgat gcactctggc	600
atggaggtag tactggctaa cggatgaactg ctgcgtaccg gtatgggtgc tctgccggac	660
ccgaagcgtc cggaactat gggctctgaag ccggaggatc agccgtggtc taaaatcgct	720
catctgttcc cgtatggctt tgggtccgtac atcgacggtc tgttctctca gtctaacaatg	780







Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala  
1 5 10 15

Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala  
35 40 45

Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr  
65 70 75 80

Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp  
100 105 110

Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu  
130 135 140

Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser  
165 170 175

Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu  
195 200 205

Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp  
225 230 235 240

Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr  
260 265 270

52



275

280

<210> 71  
<211> 852  
<212> DNA  
<213> Artificial Sequence

<400> 71  
atggcctaaaa acttctctaa cgttgaatac ccggctccgc cgcagctca caccacaaac 60  
gaatctctgc aggttctgga cctgttcaaa ctgaacggta aggttgottc tatcacccgt 120  
tcttcttctg gtatcggta cgtctggct gaagcattcg ctcaggtagg tgctgacgtt 180  
gctatctggg acaactctca cgacgtact ggtaaggctg aagctctggc taaaaaatac 240  
gggtgttaaag ttaaagctta caaggctaac gtttcttctt ctgacgctgt aaaacagacc 300  
atcgaacagc agatcaaaga cttcggtcac ctggacatcg ttgttgctaa cgtcgggtatc 360  
ccgtggacca aaggtgctta catcgaccag gacgacgata aacacttcga tcaggttggt 420  
gacgttgatc tgaaagggtg tggttatggt gctaaacacg ctggccgtca cttccgtgag 480  
cgtttcgaaa aggaaggtaa gaaaggcgt ctggttttca ccgcttctat gtctgggtcac 540  
atcgttaacg taccgcagtt tcaggctacc tacaacgctg ctaaagctgg tgttcgtcac 600  
ttcgtctaat ctctggctgt agaattcgtc ccgttcgctc gtgttaactc tgtttctccg 660  
ggctacatca acaccgaaat ctctgacttt gtaccgcagg aaactcagaa caaatgggtg 720  
tctctgggtc cgtcggggcg tgggtggcgaa actgctgaac tgggtgggtg ttacctgttt 780  
ctggcttctg acgctgggtc ttacgctacc ggactgaca tcacgttgga cgggtgggtac 840  
acctgccgt aa 852

<210> 72  
<211> 1602  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 72  
atgacagaag ataatttgc tccaatcacc tccgttaaag tagttaccga caagtgcacg 60  
tacaaggaca acgagctgct caccaagtag agctacgaaa atgctgtagt tacgaagaca 120  
gctagtggcc gcttcgatgt aacgcccact gttcaagact acgtgttcaa acttgacttg 180  
aaaaagccgg aaaaactagg aattatgctc attgggttag gtggcaacaa tggctccact 240  
ttagtggcct cggatttggc gaataagcac aatgtggagt ttcaaactaa ggaaggcgtt 300  
aagcaaccaa actacttcgg ctccatgact caatgttcta cttgaaact gggatatgat 360  
goggagggga atgacgttta tgctcctttt aactctctgt tgcccatggt tagcccaaac 420  
gactttgtcg tctctggttg ggacatcaat aacgcagatc tatacgaagc tatgcagaga 480

agtcaagttc	togaatatga	tctgcaacaa	cgcttgaagg	cgaagatgtc	cttgggtgaag	540
cctcttccct	ccatttacta	ccctgatttc	attgcagcta	atcaagatga	gagagccaat	600
aactgcatca	atttggatga	aaaaggcaac	gtaaccacga	ggggtaagtg	gacccatctg	660
caacgcatca	gacgcgatat	ccagaatttc	aaagaagaaa	acgcccttga	taaagtaatc	720
gttctttgga	ctgcaaatac	tgagaggtac	gtagaagtat	ctcctgggtg	taatgacacc	780
atggaaaacc	tcttgcagtc	tattaagaat	gaccatgaag	agattgctcc	ttccacgata	840
tttgcagcag	catctatctt	ggaaggtgtc	ccctatatta	atgggttcacc	gcagaatact	900
tttgttcccg	gcttggttca	gctggctgag	catgagggta	cattcattgc	gggagacgat	960
ctcaagtcgg	gacaaaccaa	gttgaagtct	gttctggccc	agttcttagt	ggatgcaggt	1020
attaaaccgg	tctccattgc	atcctataac	catttaggca	ataatgacgg	ttataactta	1080
tctgctccaa	aacaatttag	gtctaaggag	atttccaaaa	gttctgtcat	agatgacatc	1140
atcgctcta	atgatatctt	gtacaatgat	aaactgggta	aaaaagttga	ccactgcatt	1200
gtcatcaaat	atatgaagcc	cgtcggggac	tcaaaagtgg	caatggacga	gtattacagt	1260
gagttgatgt	taggtggcca	taaccggatt	tccattcaca	atgtttgcga	agattcttta	1320
ctggctacgc	cottgatcat	cgatctttta	gtcatgactg	agttttgtac	aagagtgtcc	1380
tataagaagg	tggaccacgt	taaagaagat	gctggcaaat	tcgagaactt	ttatccagtt	1440
ttaaccttct	tgagttactg	gttaaaaagct	ccattaacaa	gaccaggatt	tcacccggtg	1500
aatggcttaa	acaagcaaag	aaccgcctta	gaaaattttt	taagattggt	gattggattg	1560
ccttctcaaa	acgaactaag	attcgaagag	agattgttgt	aa		1602

```
<210> 73
<211> 533
<212> PRT
<213> Saccharomyces cerevisiae
```

<400> 73

Met Thr Glu Asp Asn Ile Ala Pro Ile Thr Ser Val Lys Val Val Thr  
1 5 10 15

Asp Lys Cys Thr Tyr Lys Asp Asn Glu Leu Leu Thr Lys Tyr Ser Tyr  
20 25 30

Glu Asn Ala Val Val Thr Lys Thr Ala Ser Gly Arg Phe Asp Val Thr  
35 40 45

Pro Thr Val Gln Asp Tyr Val Phe Lys Leu Asp Leu Lys Lys Pro Glu  
50 55 60

Lys Leu Gly Ile Met Leu Ile Gly Leu Gly Gly Asn Asn Gly Ser Thr  
65 70 75 80















130					135					140					
Ser 145	Trp	Phe	Ala	Asp	Ser 150	Thr	Thr	Lys	Tyr	Ser 155	Asn	Phe	Glu	Thr	Arg 160
Pro	Ala	Arg	Tyr	Val 165	Arg	Leu	Val	Ala	Ile 170	Thr	Glu	Ala	Asn	Gly 175	Gln
Pro	Trp	Thr	Ser 180	Ile	Ala	Glu	Ile	Asn 185	Val	Phe	Gln	Ala	Ser 190	Ser	Tyr
Thr	Ala	Pro 195	Gln	Pro	Gly	Leu	Gly 200	Arg	Trp	Gly	Pro	Thr 205	Ile	Asp	Leu
Pro	Ile 210	Val	Pro	Ala	Ala 215	Ala	Ala	Ile	Glu	Pro	Thr 220	Ser	Gly	Arg	Val
Leu 225	Met	Trp	Ser	Ser 230	Tyr	Arg	Asn	Asp	Ala	Phe 235	Gly	Gly	Ser	Pro	Gly 240
Gly	Ile	Thr	Leu	Thr 245	Ser	Ser	Trp	Asp	Pro 250	Ser	Thr	Gly	Ile	Val 255	Ser
Asp	Arg	Thr	Val 260	Thr	Val	Thr	Lys	His 265	Asp	Met	Phe	Cys	Pro 270	Gly	Ile
Ser	Met	Asp 275	Gly	Asn	Gly	Gln	Ile 280	Val	Val	Thr	Gly	Gly 285	Asn	Asp	Ala
Lys	Lys 290	Thr	Ser	Leu	Tyr	Asp 295	Ser	Ser	Ser	Asp	Ser 300	Trp	Ile	Pro	Gly
Pro 305	Asp	Met	Gln	Val	Ala 310	Arg	Gly	Tyr	Gln	Ser 315	Ser	Ala	Thr	Met	Ser 320
Asp	Gly	Arg	Val	Phe 325	Thr	Ile	Gly	Gly	Ser 330	Trp	Ser	Gly	Gly	Val 335	Phe
Glu	Lys	Asn	Gly 340	Glu	Val	Tyr	Ser	Pro 345	Ser	Ser	Lys	Thr	Trp 350	Thr	Ser
Leu	Pro	Asn 355	Ala	Lys	Val	Asn	Pro 360	Met	Leu	Thr	Ala	Asp 365	Lys	Gln	Gly
Leu	Tyr 370	Arg	Ser	Asp	Asn	His 375	Ala	Trp	Leu	Phe	Gly 380	Trp	Lys	Lys	Gly
Ser 385	Val	Phe	Gln	Ala	Gly 390	Pro	Ser	Thr	Ala	Met 395	Asn	Trp	Tyr	Tyr	Thr 400
Ser	Gly	Ser	Gly	Asp 405	Val	Lys	Ser	Ala	Gly 410	Lys	Arg	Gln	Ser	Asn 415	Arg
Gly	Val	Ala	Pro 420	Asp	Ala	Met	Cys	Gly 425	Asn	Ala	Val	Met	Tyr 430	Asp	Ala
Val	Lys	Gly 435	Lys	Ile	Leu	Thr	Phe	Gly 440	Gly	Ser	Pro	Asp 445	Tyr	Gln	Asp
Ser	Asp 450	Ala	Thr	Thr	Asn	Ala 455	His	Ile	Ile	Thr	Leu 460	Gly	Glu	Pro	Gly

Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg  
465 470 475 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr  
485 490 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe  
500 505 510

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn  
515 520 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro  
530 535 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr  
545 550 555 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn  
565 570 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr  
580 585 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser  
595 600 605

Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val  
610 615 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly  
625 630 635 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro  
645 650 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val  
660 665 670

Ala Ser Thr Ile Arg Val Thr Gln  
675 680

<210> 78  
<211> 2046  
<212> DNA  
<213> Artificial Sequence

<400> 78  
atgggcaagc atctgctgac tctggcactg tgtttctctt ctatcaacgc tgttgctgta 60  
accgttccgc ataaggctgt tggtagcggt atcccgaag gttctctgca gttctgtct 120  
ctgctgctt ctgctccgat cggttctgct atctctcgta acaactgggc agttacctgc 180  
gactccgcac agtctggttaa cgaatgcaac aaagctatcg acggttaaca agacactttt 240  
tggcacactt tctatggcgc taacggcgac ccgaaaccgc cgcacaccta caccatgat 300  
atgaaaacca ctcagaacgt aaacggcctg tctatgctgc cgcgccagga tggttaaccag 360

aacggttga	ttggctgtca	tgaggtatat	ctgtcttccg	atggtactaa	ctggggttct	420
ccggtagctt	ctggctcctg	gttcgctgac	tctaccacca	aatactctaa	cttcgagact	480
cgtccggcac	gctatgtacg	cctggttgct	attactgagg	caaacggcca	gcogtggacc	540
tctatcgag	aaattaacgt	tttccaggca	tcttcttaca	ccgtccgca	gccgggtctg	600
ggctcgtggg	gtccgactat	tgacctgccg	atcgttccgg	cagctgctgc	tattgagccg	660
acttctggtc	gtgttctgat	gtggtcttct	taccgtaacg	acgttttcgg	tggttctccg	720
ggcggcatca	ccctgacctc	ttcttgggat	ccgtctactg	gcacgttttc	cgatcgtaac	780
gtaactgtta	ctaagcacga	tatgttttgt	ccgggtatct	ctatggatgg	caacggccag	840
attgtagtaa	ctgggtggca	cgacgctaaa	aaaacctctc	tgtatgattc	ctcctctgat	900
tcttgatcc	cggtccgga	catgcaggta	gtcgcgggtt	atcagtcttc	cgctactatg	960
tctgatggcc	gtgttttcac	tattggtggg	tcttggtctg	gcggcgtatt	tgagaaaaac	1020
ggtgaagttt	actctccatc	ctccaaaact	tggaactccc	tgccgaacgc	taaagttaac	1080
ccgatgctga	ctgcagataa	gcagggcctg	taccgttccg	ataaccaacg	atggctgttt	1140
ggctggaaaa	aaggctccgt	atttcaggct	ggcccgctca	ctgctatgaa	ctggtactat	1200
acttctgggt	ctggcgatgt	taagtccgct	ggcaagcgtc	agtctaaccg	tggcgtagca	1260
ccgatgcta	tgtgcggtaa	cgctgttatg	tacgatgctg	taaagggcaa	gattctgact	1320
tttggtggct	ctccggacta	tcaggactcc	gacgctacta	ctaacgcaca	tatcattact	1380
ctgggtgagc	cggttacctc	tccgaacact	gtatttgcat	ctaacggcct	gtactttgct	1440
cgtacctttc	acacctctgt	agtactgccg	gatggttcca	cttttatcac	tggcggtcag	1500
cgcgcgggta	ttccgttcga	ggactctact	ccggttttca	ccccggagat	ctacgtaccg	1560
gagcaggata	ctttctacaa	gcagaaccgg	aactccattg	ttcgtgtata	ccactctatc	1620
tctctgctgc	tgccggatgg	tcgtgtatct	aacggtggtg	gtggtctgtg	tggcgactgt	1680
actactaacc	atttcgatgc	gcagattttt	acccgaact	atctgtataa	ctctaaccgt	1740
aacctggcaa	ctcgcccgaa	aattactcgc	acttctaccc	agtctgtaaa	ggtaggcggc	1800
cgtatcacca	tctctaccga	ctcttctatc	tctaaagctt	ctctgattcg	ctatgggtacc	1860
gctaccata	ctgtaaacac	tgaccagcgt	cgtatcccg	tgaccctgac	caacaacggt	1920
ggtaactctt	actcttttca	ggttccgtct	gactctgggtg	ttgctctgcc	gggttactgg	1980
atgctgttcg	ttatgaactc	tgctggtgtt	ccgtctgttg	cttctaccat	ccgtgttacc	2040
cagtag						2046

<210> 79  
<211> 681







# SEQUENCE LISTING

<110> Rozzell, J. David  
Bui, Peter  
Hua, Ling

<120> SYNTHETIC GENES FOR ENHANCED EXPRESSION

<130> B583:40608

<150> 09/494,921

<151> 2000-01-31

<160> 79

<170> PatentIn version 3.0

<210> 1

<211> 1197

<212> DNA

<213> Pseudomonas putida

<400> 1

```
atgcacggct ccaacaagct ccaggattt gccacccgcg ccattcacca tggctacgac      60
ccccaggacc acggcggcgc actggtgcc a cgggtctacc agaccgcgac gttcaccttc      120
cccaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggcggggca tttctacagc      180
cgcattctcca accccaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc      240
gaggccgggc tggcgctggc ctcgggcatg ggggcgatca cgtccacgct atggacactg      300
ctgcgccccg gtgacgaggt gctgctgggc aacaccctgt acggctgcac ctttgccctc      360
ctgcaccacg gcacggcgga gttcggggtc aagctgcgcc atgtggacat ggccgacctg      420
caggcaactg aggcggccat gacgcgggcc acccggtga tctatttcga gtcgccggcc      480
aaccccaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc      540
gcgacogtgg tggtcgacaa cacctactgc acgcogtacc tgcaacggcc actggagctg      600
ggcgccgacc tgggtggtgca ttcggccacc aagtaacctga gcggccatgg cgacatcact      660
gctggcattg tgggtggcag ccaggcactg gtggaccgta tacgtctgca gggcctcaag      720
gacatgaccg gtgcgggtgct ctgcgcccat gacgcgcgac tgttgatgcg cggcatcaag      780
accctcaacc tgcgcatgga ccgccactgc gccaacgctc aggtgctggc cgagttcctc      840
gccggcgagc cgcagggtga gctgatccat taccggggcc tggcgagctt cccgcagtac      900
accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc      960
ggcatcggtg ccggggcggc gttcatgaac gccctgcaac tgttcagccg cgcggtgagc     1020
ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcatte cagctataacc     1080
ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcggttgtc ggtggggctg     1140
```









<213> Artificial sequence

<400> 6

ggcactggaa gcggttatga ccccggttac cagtgttatc tacttcgaat ccccggttaa 60  
 cccgaacatg cacatggctg acatcgagcgt gtgtgctaaa atcgctcgta agcacggcgc 120  
 taccgtagtt gttgataaca cctactgtac tccgtacctg caacgtccgc tggaaactggg 180  
 cgctgacctg gttgttctact ccgtactata atacctgtcc ggccacggcg acatcactgc 240  
 tggcatcgta gtaggctccc aggcactggt tgacctatc cgtctgcaag gtctgaaaga 300  
 catgaccggc gctgttctgt ccccgcacga cgcagcactg ctgatgcgtg gtatcaagac 360  
 cctgaacctg cgtatggacc gtcactgtgc taacgctcag gtactggctg 410

<210> 7

<211> 430

<212> DNA

<213> Artificial sequence

<400> 7

gctgacctgc aggcactgga agcggctatg accccggcta cccgtgttat ctacttcgaa 60  
 tccccggcta acccgaacat gcacatggct gacatcgagc gtgttgctaa aatcgctcgt 120  
 aagcacggcg ctaccgtagt tgttgataac acctactgta ctccgtacct gcaacgtccg 180  
 ctggaactgg gcgctgacct ggttgttcac tccgtacta aatacctgtc cggccacggc 240  
 gacatcactg ctggcatcgt agtaggctcc caggcactgg ttgacctat ccgtctgcaa 300  
 ggtctgaaag acatgaccgg cgctgttctg tccccgcacg acgcagcact gctgatgcgt 360  
 ggtatcaaga cctgaacct gcgtatggac cgtcactgtg ctaacgctca ggtactggct 420  
 gaattcctgg 430

<210> 8

<211> 366

<212> DNA

<213> Artificial sequence

<400> 8

aattcctggc tcgtcagccg caggtagaac tgatccacta tccgggcctg gtttccttcc 60  
 cgcagtacac tctggcacgt cagcagatgt cccagccggg cggatgatc gttttcgaac 120  
 tgaagggtgg catcgccgct ggtcgtcgtt tcatgaacgc tctgcagctg ttctcccgtg 180  
 cggtttccct gggtgacgt gaatccctgg cgcagcacc ggcatccatg actcactcct 240  
 cctacactcc ggaagaacgt gcgcactacg gcattctcga aggcctgggt cgtctgtctg 300  
 ttggtctgga agacatcgat gatctgctgg cagacgttca gcaggctctg aaggctagcg 360  
 cttgag 366







gcggtttccc tgggtgacgc tgaatccctg ggcagcacc cggcatccat gactcactcc 60  
tctacactc cggaagaacg tgcgcactac ggcattctccg aaggcc 106

<210> 26  
<211> 98  
<212> DNA  
<213> Artificial Sequence

<400> 26  
caagcgctag ccttcagagc ctgctgaacg tctgccagca gatcatcgat gtcttccaga 60  
ccaacagaca gacgaaccag gccttcggag atgccgta 98

<210> 27  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<400> 27  
tggtggatcc tcaagcgcta gccttcagag cc 32

<210> 28  
<211> 1197  
<212> DNA  
<213> Artificial Sequence

<400> 28  
atgcacggct ccaacaagct ccaggattt gccaccgcg ccattcacca tggctacgac 60  
ccccaggacc acggcggcgc actggtgcc aagggtctacc agaccgcgac gttcaccttc 120  
cccaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggcggggca tttctacagc 180  
cgcatctcca accccacct caacctgctg gaagcacgca tggcctcgt ggaaggcggc 240  
gaggccgggc tggcgctggc ctcgggcatg ggggcgatca cgtccacgct atggacactg 300  
ctgcgccccg gtgacgaggt gctgctgggc aacacctgt acggctgcac ctttgcttc 360  
ctgcaccaag gcatcggcga gttcggggtc aagctgcgcc atgtggacat ggccgacctg 420  
caggcactgg aggcggccat gacgcgggc acccgtgtga tctatttcga gtgcggggc 480  
aaccocaaaca tgcacatggc cgatatgcc gccgtggcga agattgcacg caagcacggc 540  
gcgaccgtgg tggctgacaa cacctactgc acgcgtacc tgcaacgtcc actggagctg 600  
ggcgccgacc tgggtggtgca ttgggccacc aagtacctga gcggccatgg cgacatcact 660  
gctggcattg tgggtggcag ccaggcactg gtggaccgta tacgtctgca gggcctcaag 720  
gacatgaccg gtgcggtgct ctgcgcccat gacgcgcac tgttgatgcg cggcatcaag 780  
acctcaacc tgcgcatgga ccgcactgc gccaacgctc aggtgctggc cgagttcctc 840  
gcccgtcagc cgcaggtgga gctgatccat taccggggc tggcgagctt cccgcagtac 900

accctggccc gccagcagat gagccagccg ggcggcatga tgccttcga actcaagggc 960  
 ggcatcggtg ccggggcgctg ttatcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020  
 ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080  
 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcgtttgtc ggtggggctg 1140  
 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgctga 1197

<210> 29  
 <211> 1197  
 <212> DNA  
 <213> Artificial Sequence

<400> 29  
 atgcacggct ccaacaagct cccaggattt gccacccgag ccattcacca tggctacgac 60  
 ccgcaggacc acggcgggcg actggtgcca ccggtctacc agaccgagc gttcaccttc 120  
 ccgaccgtgg aatacggcg cgcgtgcttt gccggcgagc aggccgggca ttctacagc 180  
 cgcacttcca acccgacct caacctgctg gaagcagca tggcctcgtt ggaaggcggc 240  
 gaggcggggc tggcgctggc ctcgggcatg gggggcgatc cgtccacgct gtggacactg 300  
 ctgcgcccgg gtgacgaggt gctgctgggc aacacctgt acggctgcac ctttgcttc 360  
 ctgcaccacg gcatcggcga gttcggggtc aagctgcgc atgtggacat ggccgacctg 420  
 caggcactgg aggcggccat gacgcgggc acccgtgtga tctatttcga gtgcggggc 480  
 aaccgaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcag caagcacggc 540  
 ggcaccgtgg tggcgacaa cacctactgc acgcgtacc tgcaacgtcc actggagctg 600  
 ggcggcgacc tgggtgtgca ttcgccacc aagtaacctg gcggccatgg cgacatcact 660  
 gctggcattg tgggtggcag ccaggcactg gtggacgta tccgtctgca gggcctcaag 720  
 gacatgaccg gtgcggtgct ctgcggcat gacgcgcac tgttgatgcg cggcatcaag 780  
 accctcaacc tgcgcattga ccgccactgc gccaacgctc aggtgctggc cgagttcctc 840  
 gccgctcagc cgcagggtga gctgatccat taccggggc tggcgagctt cccgcagtac 900  
 accctggccc gccagcagat gagccagccg ggcggcatga tgccttcga actcaagggc 960  
 ggcatcggtg ccggggcgctg ttatcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020  
 ctggggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080  
 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcgtttgtc ggtggggctg 1140  
 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgctga 1197

<210> 30  
 <211> 1200  
 <212> DNA



<213> Artificial Sequence

<400> 30

atgggtcacg gctccaacaa actgccgggt tttgctaccc gtgctatcca ccacggctac 60  
gaccgcagg accacggcgg cgactgggtt ccgccggttt accagaccgc gaccttcacc 120  
ttcccgaccg ttgaatacgg cgctgcgtgc tttgctggcg aacaggctgg tcaacttctac 180  
tcccgtatct ccaacccgac cctgaacctg ctggaagcac gtatggcttc cctggaaggc 240  
ggcgaagctg gtctggcgct ggcttccggc atgggtgcga tcacctccac cctgtggacc 300  
ctgctgcgtc cgggtgacga agttctgctg ggcaacaccc tgtacggctg cacctttgct 360  
ttctgcacc acggcatcgg cgaattcggg gttaagctgc gtcacgttga catggctgac 420  
ctgcaggcac tggaagcggc tatgaccccg gctaccctg tttatctactt cgaatccccg 480  
gctaaccgca acatgcacat ggctgaaatc gctggcggtt cgaagatcgc acgtaagcac 540  
ggcgcgaccg ttgttggtga caacacctac tgcaccccg acctgcaacg tccgctggaa 600  
ctgggcgctg acctgggtgt tcaactccgt accaagtacc tgtccggcca cggcgacatc 660  
actgctggca tcgttggttg ctcccaggca ctgggtgacc gtatccgtct gcaaggcctg 720  
aaggacatga ccggtgcggg tctgtccccg cagcagctg cactgctgat gcgtggcatc 780  
aagaccctga acctgcgtat ggaccgtcac tgcgctaacg ctacaggttct ggctgaattc 840  
ctggctcgtc agccgcaggg tgaactgatc cactaccogg gcctggcgctc cttcccgag 900  
tacaccctgg ctgctcagca gatgtcccag ccgggcggca tgatcgcttt cgaactgaag 960  
ggcggcatcg gtgctggctg tcgtttcatg aacgctctgc agctgttctc ccgtgcgggtt 1020  
tccctgggcg aagctgaatc cctggcgag caccggcat ccatgactca ctcctcctac 1080  
accccggaag aacgtgcgca ctacggcatc tccgaaggtc tggttcgtct gtccgttggt 1140  
ctggaagaca tcgacgacct gctggctgaa gttcagcagg cactgaaggc gagtgcttga 1200

<210> 31

<211> 972

<212> DNA

<213> *Sporidiobolus salmonicolor*

<400> 31

atggctggca ctactaccct caacactggc gtttccctcg agctcgtcgg ctacggcacg 60  
tggcaggcag caccgggcga ggtgggccag ggctcaagg tcgccatcga gactggatac 120  
cgtaacctcg accttgccaa ggtctactcg aaccaacctg aggttggtgc cgccatcaag 180  
gaggctggcg tcaagcgaga ggacctcttc atcacctcga agctctggaa caactcgcac 240  
cgcccgagc aggtcgagcc tgcccttgac gacacctca aggagctcgg cctcgagtac 300  
ctcgaccttt acctcattca ctggcccgct gcgttccgc ccgagggcga catcaccag 360



Asn Phe Asp Ala Lys Met Val Asp Ala Ile Ile Glu Ala Thr Gly Val  
                     165                    170                    175  
 Thr Pro Ser Val Asn Gln Ile Glu Arg His Pro Leu Leu Leu Gln Pro  
                     180                    185                    190  
 Glu Leu Ile Ala His His Lys Ala Lys Asn Ile His Ile Thr Ala Tyr  
                     195                    200                    205  
 Ser Pro Leu Gly Asn Asn Thr Val Gly Ala Pro Leu Leu Val Gln His  
                     210                    215                    220  
 Pro Glu Ile Lys Arg Ile Ala Glu Lys Asn Gly Cys Thr Pro Ala Gln  
                     225                    230                    235                    240  
 Val Leu Ile Ala Trp Ala Ile Val Gly Gly His Ser Val Ile Pro Lys  
                     245                    250                    255  
 Ser Val Thr Pro Ser Arg Ile Gly Glu Asn Phe Lys Gln Val Ser Leu  
                     260                    265                    270  
 Ser Gln Glu Asp Val Asp Ala Val Ser Lys Leu Gly Glu Gly Ser Gly  
                     275                    280                    285  
 Arg Arg Arg Tyr Asn Ile Pro Cys Thr Tyr Ser Pro Lys Trp Asp Ile  
                     290                    295                    300  
 Asn Val Phe Gly Glu Glu Asp Glu Lys Ser Cys Lys Asn Ala Val Lys  
                     305                    310                    315                    320  
 Ile Lys

<210> 33  
 <211> 972  
 <212> DNA  
 <213> Artificial sequence

<400> 33  
 atggttggtgta ctactactct gaacactggt gcatctctgg aactggtagg ttatggtact 60  
 tggcaagctg ctccgggcga agtaggtcaa ggtgtaaaag tagctatcga aactggttat 120  
 cgtcatctgg atctggcaaa agtatactct aaccagccgg aagtaggtgc agcaatcaag 180  
 gaagctggcg ttaaactgta ggatctgttt atcacttcta aactgtggaa caactcccac 240  
 cgtccggaac aggtagaacc ggctctggat gatactctga aagaactggg cctggagtat 300  
 ctggacctgt acctgatcca ctggccggtg gcatctccgc cggaaggtga tatcactcag 360  
 aacctgttcc cgaaagctaa cgataaagaa gtaaaactgg acctggaagt ttctctggta 420  
 gacacttgga aagcaatggt aaaactgctg gatactggta aagttaaagc tatcgggtgtt 480  
 tccaactttg acgcaaaaat ggttgacgct atcatcgaag caactggcgt aactccgtct 540  
 gttaaccaga tcgaacgtca cccgctgctg ctgcagccag agctgatcgc acaccacaaa 600  
 gctaaaaaca tccacatcac cgcatactcc ccgctgggta acaacaccgt aggcgaccg 660

ctgctggtac aacacccgga aatcaaacgt atcgctgaaa aaaacggctg tactccggct 720  
caggtactga tcgcatgggc tatcgtaggt ggtcattctg ttatcccgaa atccgtaact 780  
ccgtctcgta ttggcgaaaa cttcaaacag gtttctctgt ctcaggaaga tgttgatgct 840  
gtttctaagc tgggcgaagg ttccggctgt cgtcgttata acatcccggtg cacttattcc 900  
ccgaagtggg atatcaacgt ttccggtgaa gaagatgaaa aatcctgtaa aaacgctggt 960  
aaaatcaaat aa 972

<210> 34  
<211> 1032  
<212> DNA  
<213> *Sporidiobolus salmonicolor*

<400> 34  
atggccaaaa tcgacaacgc tgtgcttccc gagggctcgc tcgtgctcgt caccggcgcc 60  
aacggcttcg tcgcttcgca cgtcgtcgaa cagctccttg aacacgggta caagggtccgt 120  
ggtacggctc gtagtgccctc caaacttgcc aacctgcaga agcgtcggga tgccaagtac 180  
cccggctcgt tcgagacggc cgtggctgag gacatgctca aacagggagc ttacgacgaa 240  
gtgatcaagg gcgcgcgcgg agttgcgcac atcgcttccg tcgtgtcctt ctgaacaag 300  
tacgacgagg ttgtcacccc cgccatcgga ggcacctca acgctctccg tgccgcgcgt 360  
gccacgccct ctgtcaagcg cttcgtcctc acctcctcga ccgtttcagc gcttatcccc 420  
aagccgaatg tcgaggggat ctacctcgac gagaagtcct ggaacctcga gagcatcgac 480  
aaggccaaga ctctccctga aagcgacccc cagaagtcgc tctgggtcta cgccgcgagc 540  
aagaccgagg cggagcttgc cgcttggaat ttcatggacg agaacaagcc gcacttcacc 600  
ctcaacgccg tcctcccca ctacacgatt gggacgatct tcgaccccgga gaccaggtcc 660  
ggctcgactt cgggctggat gatgagtctc ttcaatggcg aagtttcccc cgccctcgt 720  
ctgatgcccc ctcagtacta cgtgtcggcc gtcgacattg gtctcctgca cctcgggtgc 780  
ttggttctgc ccagatcga gcgcgcgcgc gtctacggca ccgccggcac gttcgactgg 840  
aacacgggtc tcgcgacgtt ccgcaagctg tacccgagca agacgttccc ggccgacttc 900  
cccgaccagg gccaggacct ctccaagttc gacacggccc cgagcctcga gatcctcaag 960  
agtttgggca ggcccgggtg gaggtcgatc gaggagagca tcaaggacct cgtcgggtcc 1020  
gaaaccgctt ga 1032

<210> 35  
<211> 343  
<212> PRT  
<213> *Sporidiobolus salmonicolor*

Cognitive Function		Behavioral Function		Quality of Life		Health Status		Social Function		Economic Status	
Pre-Intervention	Post-Intervention	Pre-Intervention	Post-Intervention	Pre-Intervention	Post-Intervention	Pre-Intervention	Post-Intervention	Pre-Intervention	Post-Intervention	Pre-Intervention	Post-Intervention
10.5	11.2	12.3	13.1	14.5	15.2	16.8	17.5	18.9	19.6	20.1	20.8
11.2	12.1	13.4	14.2	15.6	16.3	17.9	18.6	19.8	20.5	21.2	21.9
12.1	13.0	14.2	15.1	16.3	17.2	18.4	19.1	20.3	21.0	21.7	22.4
13.0	13.9	15.1	16.0	17.2	18.1	19.3	20.0	21.2	21.9	22.6	23.3
13.9	14.8	16.0	16.9	18.1	19.0	20.2	20.9	22.1	22.8	23.5	24.2
14.8	15.7	16.9	17.8	19.0	19.9	21.1	21.8	23.0	23.7	24.4	25.1
15.7	16.6	17.8	18.7	19.9	20.8	22.0	22.7	23.9	24.6	25.3	26.0
16.6	17.5	18.7	19.6	20.8	21.7	22.9	23.6	24.8	25.5	26.2	26.9
17.5	18.4	19.6	20.5	21.7	22.6	23.8	24.5	25.7	26.4	27.1	27.8
18.4	19.3	20.5	21.4	22.6	23.5	24.7	25.4	26.6	27.3	28.0	28.7
19.3	20.2	21.4	22.3	23.5	24.4	25.6	26.3	27.5	28.2	28.9	29.6
20.2	21.1	22.3	23.2	24.4	25.3	26.5	27.2	28.4	29.1	29.8	30.5
21.1	22.0	23.2	24.1	25.3	26.2	27.4	28.1	29.3	30.0	30.7	31.4
22.0	22.9	24.1	25.0	26.2	27.1	28.3	29.0	30.2	30.9	31.6	32.3
22.9	23.8	25.0	25.9	27.1	28.0	29.2	29.9	31.1	31.8	32.5	33.2
23.8	24.7	25.9	26.8	28.0	28.9	30.1	30.8	32.0	32.7	33.4	34.1
24.7	25.6	26.8	27.7	28.9	29.8	31.0	31.7	32.9	33.6	34.3	35.0
25.6	26.5	27.7	28.6	29.8	30.7	31.9	32.6	33.8	34.5	35.2	35.9
26.5	27.4	28.6	29.5	30.7	31.6	32.8	33.5	34.7	35.4	36.1	36.8
27.4	28.3	29.5	30.4	31.6	32.5	33.7	34.4	35.6	36.3	37.0	37.7
28.3	29.2	30.4	31.3	32.5	33.4	34.6	35.3	36.5	37.2	37.9	38.6
29.2	30.1	31.3	32.2	33.4	34.3	35.5	36.2	37.4	38.1	38.8	39.5
30.1	31.0	32.2	33.1	34.3	35.2	36.4	37.1	38.3	39.0	39.7	40.4
31.0	31.9	33.1	34.0	35.2	36.1	37.3	38.0	39.2	39.9	40.6	41.3
31.9	32.8	34.0	34.9	36.1	37.0	38.2	38.9	40.1	40.8	41.5	42.2
32.8	33.7	34.9	35.8	37.0	37.9	39.1	39.8	41.0	41.7	42.4	43.1
33.7	34.6	35.8	36.7	37.9	38.8	39.9	40.6	41.8	42.5	43.2	43.9
34.6	35.5	36.7	37.6	38.8	39.7	40.9	41.6	42.8	43.5	44.2	44.9
35.5	36.4	37.6	38.5	39.7	40.6	41.8	42.5	43.7	44.4	45.1	45.8
36.4	37.3	38.5	39.4	40.6	41.5	42.7	43.4	44.6	45.3	46.0	46.7
37.3	38.2	39.4	40.3	41.5	42.4	4					

15

Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp  
 325 330 335

Leu Val Gly Ser Glu Thr Ala  
 340

<210> 36  
 <211> 1032  
 <212> DNA  
 <213> Artificial Sequence

<400> 36  
 atggctaaaa tcgataacgc agttctgccg gaaggttccc tggttctggt taccggtgct 60  
 aacggttttcg ttggttccca cgttggtgaa cagctgctgg aacacggtta caaagtctcg 120  
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacgttgga cgctaaatac 180  
 ccgggtcgtt tcgaaaccgc tgttggtgaa gacatgctga aacaggtgc ttacgacgaa 240  
 gttatcaaag gtgctgctgg tgttgctcac atcgcttcog ttgtttcctt ctccaacaaa 300  
 tacgacgaag ttgttaccgc ggctatcggg ggtaccctga acgctctgog tgctgctgct 360  
 gctaccccggt ccgttaaaccg tttcgttctg acctcctcca ccgtttccgc tctgatcccg 420  
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480  
 aaagctaaaa cctgcccga atccgaccog cagaaatccc tgtgggtata cgctgcatcc 540  
 aagaccgaag ctgaactggc tgcattgaaa tttatggatg agaacaagcc aacttcaact 600  
 ctgaacgctg tactgcaaaa ctacactatt ggactatct tcgatccgga aactcagtcc 660  
 ggttccacct ccggttggtat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720  
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggttg 780  
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta ctgctggtac tttcgattgg 840  
 aacaccgttc tggctacctt ccgtaaactg taccgctcca aaaccttccc ggctgacttc 900  
 ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960  
 tctctgggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020  
 gaaaccgctt aa 1032

<210> 37  
 <211> 343  
 <212> PRT  
 <213> Artificial Sequence

<400> 37

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu  
 1 5 10 15

Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu



<210> 38  
 <211> 942  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 38  
 atgggtcctg ctacgttaaa gaattcttct gctacattaa aactaaatac tgggtgcctcc 60  
 attccagtgt tgggtttcgg cacttggcgt tccgttgaca ataaoggtta ccattctgta 120  
 attgcagctt tgaaagctgg atacagacac attgatgctg cggctatcta tttgaatgaa 180  
 gaagaagttg gcagggctat taaagattcc ggagtcctc gtgaggaaat ttttattact 240  
 actaagcttt ggggtacgga acaacgtgat ccggaagctg ctctaaacaa gtctttgaaa 300  
 agactaggct tggattatgt tgacctatat ctgatgcatt ggccagtgcc tttgaaaacc 360  
 gacagagtta ctgatggtaa cgttctgtgc attccaacat tagaagatgg cactgttgac 420  
 atcgatacta aggaatggaa ttttatcaag acgtgggagt tgatgcaaga gttgccaaag 480  
 acggggcaaaa ctaaagccgt tgggtgtctct aattttttcta ttaacaacat taaagaatta 540  
 ttagaatctc caaataacaa ggtggtacca gctactaatc aaattgaaat tcatccattg 600  
 ctaccacaag acgaattgat tgccttttgt aaggaaaagg grattgttgt tgaagcctac 660  
 tcaccatttg ggagtgctaa tgctccttta ctaaaagagc aagcaattat tgatatggct 720  
 aaaaagcacg gcgttgagcc agcacagctt attatcagtt ggagtattca aagaggctac 780  
 gttgttcttg ccaaatecgt taatcctgaa agaattgtat ccaattttta gattttcact 840  
 ctgcctgagg atgatttcaa gactattagt aacctatcca aagtgcattg tacaaagaga 900  
 gtcgttgata tgaagtgggg atccttccca attttccaat ga 942

<210> 39  
 <211> 313  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 39  
 Met Gly Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn  
 1 5 10 15  
 Thr Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val  
 20 25 30  
 Asp Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr  
 35 40 45  
 Arg His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly  
 50 55 60  
 Arg Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr  
 65 70 75 80





cgtctgggtc tggactacgt agacctgtac ctgatgcact ggccggtacc gctgaaaact 360  
gaccgtgtta ctgatggtaa cgttctgtgt attccgactc tggaagacgg tactgtagac 420  
atcgacacta aggaatggaa cttcatcaag acttggaac tgatgcagga actgccgaaa 480  
actggtaaaa ctaaagcagt aggtgtttcc aacttctcta tcaacaacat caaagaactg 540  
ctggaatctc cgaacaacaa agtagtaccg gcaactaacc agatcgaaat ccaccgctg 600  
ctgccgcagg acgaactgat cgcattctgc aaagagaaag gtatcgtagt agaagcatac 660  
tctccgttcg gctctgcaaa cgcaccgctg ctgaaagaac aggcaatcat cgacatggca 720  
aagaaacacg gtgtagaacc ggacacagctg atcatctctt ggtctatcca gcgtgggttac 780  
gtagtactgg caaaatctgt aaaccggaa cgtatcgat ctaacttcaa aatcttcaact 840  
ctgccggaag acgacttcaa aactatctct aacctgtcca aagttcacgg tactaaacgt 900  
gtagtagaca tgaaatgggg ttctttcccg atcttcagtt aa 942

<210> 41  
<211> 939  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<400> 41  
atgctgtcta ctttacatga ttctacgaaa atcctttctc taaatactgg agcccaaact 60  
cctcaaatag gtttaggtac gtggcagctg aaagagaacg atgcttataa ggctgtttta 120  
accgctttga aagatggcta ccgacacatt gatactgctg ctatttaccg taatgaagac 180  
caagtcggtc aagccatcaa ggattcaggt gttcctcggg aagaaatctt tgttactaca 240  
aagttatggt gtacacaaca ccacgaacct gaagtagcgc tggatcaatc actaaagagg 300  
ttaggattgg actacgtaga cttatatattg atgcattggc ctgccagatt agatccagcc 360  
tacatcaaaa atgaagacat cttgagtgtg ccaacaaaga aggatgggtc tcgtgcagtg 420  
gatatcacca attggaattt catcaaaacc tgggaattaa tgcaggaact accaaagact 480  
ggtaaaacta aggcggttgg agtctccaac ttttctataa ataacctgaa agatctatta 540  
gcatctcaag gtaataagct tacgccagct gctaaccaag tcgaaatata tccattacta 600  
cctcaagacg aattgattaa tttttgtaaa agtaaaggca ttgtggttga agcttattct 660  
ccgttaggta gtaccgatgc tccactattg aaggaaccgg ttatccttga aattgcgaag 720  
aaaaataacg ttcaaccogg acacgttggt attagctggc acgtccaaag aggttatggt 780  
gtcttgccaa aatctgtgaa tcccgatcga atcaaaacga acaggaaaat atttactttg 840  
tctactgagg actttgaagc tatcaataac atatcgaagg aaaagggcga aaaaagggtt 900  
gtacatccaa attgggtctcc tttcgaagta ttcaagtaa 939

<210> 42  
 <211> 312  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 42

Met	Pro	Ala	Thr	Leu	His	Asp	Ser	Thr	Lys	Ile	Leu	Ser	Leu	Asn	Thr
1				5					10					15	
Gly	Ala	Gln	Ile	Pro	Gln	Ile	Gly	Leu	Gly	Thr	Trp	Gln	Ser	Lys	Glu
		20						25					30		
Asn	Asp	Ala	Tyr	Lys	Ala	Val	Leu	Thr	Ala	Leu	Lys	Asp	Gly	Tyr	Arg
	35						40					45			
His	Ile	Asp	Thr	Ala	Ala	Ile	Tyr	Arg	Asn	Glu	Asp	Gln	Val	Gly	Gln
	50					55					60				
Ala	Ile	Lys	Asp	Ser	Gly	Val	Pro	Arg	Glu	Glu	Ile	Phe	Val	Thr	Thr
65					70					75					80
Lys	Leu	Trp	Cys	Thr	Gln	His	His	Glu	Pro	Glu	Val	Ala	Leu	Asp	Gln
			85					90						95	
Ser	Leu	Lys	Arg	Leu	Gly	Leu	Asp	Tyr	Val	Asp	Leu	Tyr	Leu	Met	His
			100					105					110		
Trp	Pro	Ala	Arg	Leu	Asp	Pro	Ala	Tyr	Ile	Lys	Asn	Glu	Asp	Ile	Leu
		115					120						125		
Ser	Val	Pro	Thr	Lys	Lys	Asp	Gly	Ser	Arg	Ala	Val	Asp	Ile	Thr	Asn
	130					135						140			
Trp	Asn	Phe	Ile	Lys	Thr	Trp	Glu	Leu	Met	Gln	Glu	Leu	Pro	Lys	Thr
145					150					155				160	
Gly	Lys	Thr	Lys	Ala	Val	Gly	Val	Ser	Asn	Phe	Ser	Ile	Asn	Asn	Leu
				165					170					175	
Lys	Asp	Leu	Leu	Ala	Ser	Gln	Gly	Asn	Lys	Leu	Thr	Pro	Ala	Ala	Asn
			180					185					190		
Gln	Val	Glu	Ile	His	Pro	Leu	Leu	Pro	Gln	Asp	Glu	Leu	Ile	Asn	Phe
	195						200					205			
Cys	Lys	Ser	Lys	Gly	Ile	Val	Val	Glu	Ala	Tyr	Ser	Pro	Leu	Gly	Ser
	210					215					220				
Thr	Asp	Ala	Pro	Leu	Leu	Lys	Glu	Pro	Val	Ile	Leu	Glu	Ile	Ala	Lys
225					230					235					240
Lys	Asn	Asn	Val	Gln	Pro	Gly	His	Val	Val	Ile	Ser	Trp	His	Val	Gln
			245						250					255	
Arg	Gly	Tyr	Val	Val	Leu	Pro	Lys	Ser	Val	Asn	Pro	Asp	Arg	Ile	Lys
			260					265					270		
Thr	Asn	Arg	Lys	Ile	Phe	Thr	Leu	Ser	Thr	Glu	Asp	Phe	Glu	Ala	Ile

275	280	285	
Asn Asn Ile Ser Lys Glu Lys Gly Glu Lys Arg Val Val His Pro Asn			
290	295	300	
Trp Ser Pro Phe Glu Val Phe Lys			
305	310		

<210> 43  
 <211> 942  
 <212> DNA  
 <213> Artificial Sequence

<400> 43  
 atgggcccag ctactctgca cgactctacc aaaattctgt ctctgaacac cggtgctcaa 60  
 atcccgcaaa tcggcctggg tacttggcaa tctaaagaaa acgacgcata caaggctggt 120  
 ctgactgctc tgaaggatgg ctatcgtcac attgatactg ctgctattta tcgtaacgag 180  
 gaccaggtag gtcaggcaat caaggactct ggcgttcgc gtgaggaaat cttcgtaact 240  
 accaaactgt ggtgcactca gcatcatgaa ccggaagtag cactggatca atctctgaag 300  
 cgtctgggtc tggactatgt tgatctgtac ctgatgcatt ggccggcgcg cctggacca 360  
 gcgtatatta aaaacgaaga tatcctgtct gttccgacta agaaagacgg ctctcgtgct 420  
 gttgacatca ctaactggaa cttcatcaag acctgggaac tgatgcagga actgccgaag 480  
 actggtaaaa ctaaagctgt tggcgtatct aacttctcca tcaacaacct gaaggacctg 540  
 ctggcatccc agggcaacaa gctgactccg gctgctaacc aagtagagat ccaccgctg 600  
 ctgccgcagg acgaactgat caacttctgt aaatctaaag gcattgtagt tgaagcatat 660  
 tctcogctgg gttctaccga tgcgccactg ctgaaagagc cggtaatcct ggagatcgcg 720  
 aagaaaaaca acgtacaacc aggtcatgta gtaatctctt ggcacgtaca gcgcggctac 780  
 gtagttctgc cgaagtctgt aaaccgggat cgtatcaaaa ctaaccgtaa aatctttacc 840  
 ctgtccacog aagatttcga agcaatcaac aacatctcca aggaaaagg cgagaaacgt 900  
 gtagttcacc caaactggtc cccgtttgaa gtattcaagt aa 942

<210> 44  
 <211> 313  
 <212> PRT  
 <213> Artificial Sequence

<400> 44

Met Gly Pro Ala Thr Leu His Asp Ser Thr Lys Ile Leu Ser Leu Asn	
1 5 10 15	
Thr Gly Ala Gln Ile Pro Gln Ile Gly Leu Gly Thr Trp Gln Ser Lys	
20 25 30	
Glu Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr	

35	40	45
Arg His Ile Asp Thr Ala	Ala Ile Tyr Arg Asn	Glu Asp Gln Val Gly
50	55	60
Gln Ala Ile Lys Asp Ser	Gly Val Pro Arg Glu	Glu Ile Phe Val Thr
65	70	75
Thr Lys Leu Trp Cys Thr	Gln His His Glu	Pro Glu Val Ala Leu Asp
	85	90
Gln Ser Leu Lys Arg Leu	Gly Leu Asp Tyr Val	Asp Leu Tyr Leu Met
	100	105
His Trp Pro Ala Arg Leu	Asp Pro Ala Tyr Ile	Lys Asn Glu Asp Ile
	115	120
Leu Ser Val Pro Thr Lys	Lys Asp Gly Ser Arg	Ala Val Asp Ile Thr
	130	135
Asn Trp Asn Phe Ile Lys	Thr Trp Glu Leu Met	Gln Glu Leu Pro Lys
	145	150
Thr Gly Lys Thr Lys Ala	Val Gly Val Ser Asn	Phe Ser Ile Asn Asn
	165	170
Leu Lys Asp Leu Leu Ala	Ser Gln Gly Asn Lys	Leu Thr Pro Ala Ala
	180	185
Asn Gln Val Glu Ile His	Pro Leu Leu Pro Gln	Asp Glu Leu Ile Asn
	195	200
Phe Cys Lys Ser Lys Gly	Ile Val Val Glu Ala	Tyr Ser Pro Leu Gly
	210	215
Ser Thr Asp Ala Pro Leu	Leu Lys Glu Pro Val	Ile Leu Glu Ile Ala
	225	230
Lys Lys Asn Asn Val Gln	Pro Gly His Val Val	Ile Ser Trp His Val
	245	250
Gln Arg Gly Tyr Val Val	Leu Pro Lys Ser Val	Asn Pro Asp Arg Ile
	260	265
Lys Thr Asn Arg Lys Ile	Phe Thr Leu Ser Thr	Glu Asp Phe Glu Ala
	275	280
Ile Asn Asn Ile Ser Lys	Glu Lys Gly Glu Lys	Arg Val Val His Pro
	290	295
Asn Trp Ser Pro Phe Glu	Val Phe Lys	
	305	310

<210> 45  
 <211> 1029  
 <212> DNA  
 <213> Saccharomyces cerevisiae

<400> 45  
 atgtcagttt tcgtttcagg tgctaacggg ttcattgccc aacacattgt cgatctcctg

ttgaaggaag	actataaggt	catcggttct	gccagaagtc	aagaaaaggc	cgagaattta	120
acggaggcct	ttggtaacaa	cccaaaattc	tccatggaag	ttgtcccaga	catatctaag	180
ctggacgcac	ttgaccatgt	tttccaaaag	cacggcaagg	atatcaagat	agttctacat	240
acggcctctc	cattctgctt	tgatatcact	gacagtgaac	gcgatttatt	aattcctgct	300
gtgaacggtg	ttaagggaat	tctccactca	attaaaaaat	acgccgctga	ttctgtagaa	360
cgtgtagttc	tcacctcttc	ttatgcagct	gtgttcgata	tggcaaaaga	aaacgataag	420
tctttaacat	ttaacgaaga	atcctggaac	ccagctacct	gggagagttg	ccaaagtgcac	480
ccagttaacg	cctactgtgg	ttctaagaag	tttgcctgaa	aagcagcttg	ggaatttcta	540
gaggagaata	gagactctgt	aaaattcgaa	ttaactgcgc	ttaaccagct	ttacgttttt	600
ggtccgcaaa	tgtttgacaa	agatgtgaaa	aaacacttga	acacatcttg	cgaactcgtc	660
aacagcttga	tgcatttatt	accagaggac	aagataccgg	aactatttgg	tggatacatt	720
gatgttcgtg	atgttgcaaa	ggctcattta	gttgcccttc	aaaagaggga	aacaattggt	780
caaagactaa	tcgtatcgga	ggccagattt	actatgcagg	atgttctcga	tatccttaac	840
gaagacttcc	ctgttctaaa	aggcaatatt	ccagtgggga	aaccagggtc	tgggtgctacc	900
cataacaccc	ttggtgctac	tcttgataat	aaaaagagta	agaaattggt	aggtttcaag	960
ttcaggaact	tgaaagagac	cattgacgac	actgcctccc	aaattttaaa	atttgagggc	1020
agaatataa						1029

```
<210> 46
<211> 342
<212> PRT
<213> Saccharomyces cerevisiae

<400> 46
```

Met	Ser	Val	Phe	Val	Ser	Gly	Ala	Asn	Gly	Phe	Ile	Ala	Gln	His	Ile
1				5					10					15	
Val	Asp	Leu	Leu	Leu	Lys	Glu	Asp	Tyr	Lys	Val	Ile	Gly	Ser	Ala	Arg
			20					25					30		
Ser	Gln	Glu	Lys	Ala	Glu	Asn	Leu	Thr	Glu	Ala	Phe	Gly	Asn	Asn	Pro
		35					40					45			
Lys	Phe	Ser	Met	Glu	Val	Val	Pro	Asp	Ile	Ser	Lys	Leu	Asp	Ala	Phe
	50					55					60				
Asp	His	Val	Phe	Gln	Lys	His	Gly	Lys	Asp	Ile	Lys	Ile	Val	Leu	His
65					70					75					80
Thr	Ala	Ser	Pro	Phe	Cys	Phe	Asp	Ile	Thr	Asp	Ser	Glu	Arg	Asp	Leu
				85					90					95	
Leu	Ile	Pro	Ala	Val	Asn	Gly	Val	Lys	Gly	Ile	Leu	His	Ser	Ile	Lys



cacactgcat ctccattctg ttttgacatc actgattctg agcgcgacct gctgattccg 300  
 gctgttaacg gtgttaaagg tattctgcac totattaaga aatatgctgc tgattccgta 360  
 gaacgcgtag ttctgacttc ctcttatgct gcagtattcg atatggctaa agagaacgac 420  
 aaatccctga cttttaacga agaattcttg aaccgggcta cctgggaatc ttgccagtct 480  
 gacccggtta acgcttattg tggctctaag aagtttgctg aaaaagctgc ttgggaattc 540  
 ctggaagaaa accgtgactc tgtaaagttc gagctgaccg ctgtaaaccg ggtatacgtt 600  
 tttggcccg c agatgttcga taaagatgta aagaagcacc tgaacacttc ctgtgaactg 660  
 gtaaactctc tgatgcacct gtctccagaa gataaaatcc cggagctggt cggcggttac 720  
 atcgacgttc gtgacgtagc aaaagcacat ctggttagctt tccagaagcg tgagactatc 780  
 ggccagcgtc tgattgttcc cgaggctcgt ttcacocatgc aggatgttct ggatattctg 840  
 aacgaagact tcccgggtact gaaaggtaac attccgggtg gtaaaccagg ctctggtgca 900  
 actcataaca ctctgggtgc aactctggat aacaagaagt ctaagaaact gctgggtttt 960  
 aaattccgta acctgaaaga aactattgac gacactgcat ctcagatcct gaaattcgaa 1020  
 ggtcgcactt aa 1032

<210> 48  
 <211> 343  
 <212> PRT  
 <213> Artificial Sequence

<400> 48

Met Gly Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His  
 1 5 10 15

Ile Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala  
 20 25 30

Arg Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn  
 35 40 45

Pro Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala  
 50 55 60

Phe Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu  
 65 70 75 80

His Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp  
 85 90 95

Leu Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile  
 100 105 110

Lys Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Leu Thr Ser Ser  
 115 120 125

Tyr Ala Ala Val Phe Asp Met Ala Lys Glu Asn Asp Lys Ser Leu Thr



130	135	140
Phe Asn Glu Glu Ser Trp Asn Pro Ala Thr Trp Glu Ser Cys Gln Ser 145 150 155 160		
Asp Pro Val Asn Ala Tyr Cys Gly Ser Lys Lys Phe Ala Glu Lys Ala 165 170 175		
Ala Trp Glu Phe Leu Glu Glu Asn Arg Asp Ser Val Lys Phe Glu Leu 180 185 190		
Thr Ala Val Asn Pro Val Tyr Val Phe Gly Pro Gln Met Phe Asp Lys 195 200 205		
Asp Val Lys Lys His Leu Asn Thr Ser Cys Glu Leu Val Asn Ser Leu 210 215 220		
Met His Leu Ser Pro Glu Asp Lys Ile Pro Glu Leu Phe Gly Gly Tyr 225 230 235 240		
Ile Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln Lys 245 250 255		
Arg Glu Thr Ile Gly Gln Arg Leu Ile Val Ser Glu Ala Arg Phe Thr 260 265 270		
Met Gln Asp Val Leu Asp Ile Leu Asn Glu Asp Phe Pro Val Leu Lys 275 280 285		
Gly Asn Ile Pro Val Gly Lys Pro Gly Ser Gly Ala Thr His Asn Thr 290 295 300		
Leu Gly Ala Thr Leu Asp Asn Lys Lys Ser Lys Lys Leu Leu Gly Phe 305 310 315 320		
Lys Phe Arg Asn Leu Lys Glu Thr Ile Asp Asp Thr Ala Ser Gln Ile 325 330 335		
Leu Lys Phe Glu Gly Arg Ile 340		

<210> 49  
 <211> 987  
 <212> DNA  
 <213> Artificial Sequence (isoleucine codon added)

<400> 49  
 atgatttcctt cactgggttac tcttaataac ggtctgaaaa tgccoctagt cggcttaggg 60  
 tgctggaaaa ttgacaaaaa agtctgtgcg aatcaaattt atgaagctat caaattaggc 120  
 taccgtttat tcgatggtgc ttgcgactac ggcaacgaaa aggaagttgg tgaaggtatc 180  
 aggaaagcca tctccgaagg tcttgtttct agaaaggata tatttgttgt ttcaaagtta 240  
 tggaacaatt ttcaccatcc tgatcatgta aaattagctt taaagaagac cttaagcgat 300  
 atgggacttg attatttaga cctgtattat attcacttcc caatgcctt caaatatggt 360  
 ccatttgaag agaaataccc tccaggattc tatacggggcg cagatgacga gaagaaaggt 420

cacatcacgc aagcacatgt accaatcata gatacgtacc gggctctgga agaattgtgtt 480  
gatgaaggct tgattaagtc tattggtgtt tccaactttc aggggaagctt gattcaagat 540  
ttattacgtg gttgtagaat caagcccggtg gctttgcaaa ttgaacaoca tccttatttg 600  
actcaagaac acctagttga gttttgtaaa ttacacgata tccaagtagt tgcttactcc 660  
tccttcggtc ctcaatcatt cattgagatg gacttacagt tggcaaaaac cacgccaact 720  
ctgttcgaga atgatgtaat caagaaggct tcacaaaacc atccaggcag taccacttcc 780  
caagtattgc ttagatgggc aactcagaga ggcattgccc tcattccaaa atcttccaag 840  
aaggaaaggt tacttggcaa cctagaaatc gaaaaaaagt tcaatttaac ggagcaagaa 900  
ttgaaggata tttctgcact aaatgccaac atcagattta atgatccatg gacctggttg 960  
gatggtaaat tccccacttt tgcttga 987

<210> 50

<211> 328

<212> PRT

<213> Artificial Sequence (isoleucine added at position 2)

<400> 50

Met Ile Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu  
1 5 10 15  
Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln  
20 25 30  
Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys  
35 40 45  
Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile  
50 55 60  
Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu  
65 70 75 80  
Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys  
85 90 95  
Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His  
100 105 110  
Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro  
115 120 125  
Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu  
130 135 140  
Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val  
145 150 155 160  
Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser  
165 170 175

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu  
180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe  
195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro  
210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr  
225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala  
325

<210> 51  
<211> 987  
<212> DNA  
<213> Artificial Sequence

<400> 51  
atgggctctt ctctggtaac tctgaacaac ggtctgaaaa tgccgctggt aggcctgggc 60  
tgctggaaaa tcgataagaa agtatgtgct aaccaaattt atgaggctat caaactgggc 120  
tatagcctgt tcgacggtgc ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180  
cgtaaagcta tctctgaagg tctggtatct cgtaaggata tctttgtagt atctaagctg 240  
tggaacaact ttcatacccc ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300  
atgggtcttg attatctgga tctgtactat atccactttc cgatcgcatt taaatacgta 360  
ccgttcgaag aaaaatatcc gccgggcttt tacactgggtg cagacgacga aaagaagggt 420  
cacatcactg aagctcacgt accgatcatc gacacttacc gtgctctgga ggaatgtgta 480  
gacgaaggtc tgatcaaate tatcggtgta tctaacttcc agggttctct gatccaggat 540  
ctgctgcgtg gttgccgtat caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600  
aaccaggaac aactgggtga attctgcaaa ctgcacgata tccaagtagt agcatactct 660  
tctttcggtc cgcagtcttt catcgaaatg gacctgcagc tggctaagac caccgccgact 720  
ctgttcgaaa acgacgtaat caagaaagta tctcagaacc acccgggctc tactacctct 780

cagggtactgc tgcgttgggc tactcagcgt ggcacgcgtg ttatcccgaa atcttctaag 840  
aaagaacgtc tgctgggtaa cctggaaatc gaaaagaaat tcactctgac cgaacaggaa 900  
ctgaaagata tctctgctct gaacgctaac atccggttca acgatccgtg gacctggctg 960  
gatggtaaata tcccgaacttt cgcttaa 987

<210> 52  
<211> 328  
<212> PRT  
<213> Artificial Sequence

<400> 52

Met Gly Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu  
1 5 10 15

Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln  
20 25 30

Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys  
35 40 45

Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile  
50 55 60

Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu  
65 70 75 80

Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys  
85 90 95

Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His  
100 105 110

Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro  
115 120 125

Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu  
130 135 140

Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val  
145 150 155 160

Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser  
165 170 175

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu  
180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe  
195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro  
210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr  
225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly  
                           245  250  255  
 Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile  
                           260  265  270  
 Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu  
                           275  280  285  
 Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile  
                           290  295  300  
 Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu  
                           305  310  315  320  
 Asp Gly Lys Phe Pro Thr Phe Ala  
   325

<210> 53  
 <211> 1461  
 <212> DNA  
 <213> Sus scrofa

<400> 53  
 atgaatgccg gcgatttccg tcgacgcggc aaagaaatgg tggattacat ggccggattac 60  
 ctggaaggca tcgaaggtcg tcaggtgtac ccggatgtgc agccggggta cctgcgtccg 120  
 ctgatcccgg cgaccgcccc gcaggaaccg gataccttcg aagatatact gcaggatgtg 180  
 gaaaaaatca tcatgccggg ggtgaccac tggcacagcc cgtacttctt cgcgtacttc 240  
 ccgaccgcca gcagctaccc ggcgatgtcg gcggatatgc tgtgcgggtg gatcggtatg 300  
 atcggtttca gctggggcgc tagcccgccg tgcaccgaac tcgagaccgt gatgatggat 360  
 tggctgggca aaatgctcca gcttcggaa gcgttcctgg cgggcgaagc cgggtgaaggc 420  
 ggccggcgtg tccagggtag cgcagcgaa gccaccctgg tggcgctgct ggccggcgcgt 480  
 accaaagtgg tgcgacgtct gcaagcggcg agcccgggcc tgaccaggg cgcggtgctg 540  
 gaaaaactag tggcgtagc gagtgatcag gcgcacagca gcgtggaacg tgccggcctg 600  
 atcgccggcg tgaaactgaa agcgatccc agcgatggca aattcgcgat gcgtgcgagc 660  
 gcgctgcagg aggcctgga gagagacaag gctgccggcc tgattccttt ctctgtggtg 720  
 gctacgtctg ggaccacatc gtgctgctcc tttgacaatc tcttagaagt gggaccatc 780  
 tgtcacgaag aggacatatg gctgcacgtg gatgctgct acgcaggcag tgccttcac 840  
 tgccctgagt tccggcacct gctgaatgga gtggagtttg cagattcatt taactttaat 900  
 cccacaaaat ggctcttggg gaattttgac tgctcggcta tgtgggtgaa aaggagaacg 960  
 gacctgactg gagccttcaa attggacccc gtgtacttaa agcacagcca ccagggtctg 1020  
 gggcttatca cggactacag gcaactggcag ctgccactgg gtcggcgatt ccggtccctg 1080









	20		25		30	
Asp Val Gln Pro Gly Tyr Leu Arg Pro Leu Ile Pro Ala Thr Ala Pro	35	40	45			
Gln Glu Pro Asp Thr Phe Glu Asp Ile Leu Gln Asp Val Glu Lys Ile	50	55	60			
Ile Met Pro Gly Val Thr His Trp His Ser Pro Tyr Phe Phe Ala Tyr	65	70	75	80		
Phe Pro Thr Ala Ser Ser Tyr Pro Ala Met Leu Ala Asp Met Leu Cys	85	90	95			
Gly Ala Ile Gly Cys Ile Gly Phe Ser Trp Ala Ala Ser Pro Ala Cys	100	105	110			
Thr Glu Leu Glu Thr Val Met Met Asp Trp Leu Gly Lys Met Leu Gln	115	120	125			
Leu Pro Glu Ala Phe Leu Ala Gly Glu Ala Gly Glu Gly Gly Gly Val	130	135	140			
Ile Gln Gly Ser Ala Ser Glu Ala Thr Leu Val Ala Leu Leu Ala Ala	145	150	155	160		
Arg Thr Lys Val Val Arg Arg Leu Gln Ala Ala Ser Pro Gly Leu Thr	165	170	175			
Gln Gly Ala Val Leu Glu Lys Leu Val Ala Tyr Ala Ser Asp Gln Ala	180	185	190			
His Ser Ser Val Glu Arg Ala Gly Leu Ile Gly Gly Val Lys Leu Lys	195	200	205			
Ala Ile Pro Ser Asp Gly Lys Phe Ala Met Arg Ala Ser Ala Leu Gln	210	215	220			
Glu Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Val	225	230	235	240		
Val Ala Thr Leu Gly Thr Thr Ser Cys Cys Ser Phe Asp Asn Leu Leu	245	250	255			
Glu Val Gly Pro Ile Cys His Glu Glu Asp Ile Trp Leu His Val Asp	260	265	270			
Ala Ala Tyr Ala Gly Ser Ala Phe Ile Cys Pro Glu Phe Arg His Leu	275	280	285			
Leu Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys	290	295	300			
Trp Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Arg Arg	305	310	315	320		
Thr Asp Leu Thr Gly Ala Phe Lys Leu Asp Pro Val Tyr Leu Lys His	325	330	335			
Ser His Gln Gly Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Leu	340	345	350			



ggtggtgatg tttggttccc acaaccagct ccaaaggatc acctatggag agatatgaga 900  
 aataaatatg gtgctggttaa tgccatgact cctcactact ctggtactac tttagacgct 960  
 caaacaagat acgctgaagg tactaaaaat attttggaaat cattctttac cggtaaattt 1020  
 gattacagac cacaagatat tatcttatta aatggtgaat acgttactaa agcttacggt 1080  
 aaacacgata agaaataa 1098

<210> 58  
 <211> 365  
 <212> PRT  
 <213> Candida boidinii

<400> 58

Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala  
 1 5 10 15  
 Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala  
 20 25 30  
 Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys  
 35 40 45  
 Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile  
 50 55 60  
 Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu  
 65 70 75 80  
 Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser  
 85 90 95  
 Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser  
 100 105 110  
 Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val  
 115 120 125  
 Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu  
 130 135 140  
 Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala  
 145 150 155 160  
 Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile  
 165 170 175  
 Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu  
 180 185 190  
 Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val  
 195 200 205  
 Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp  
 210 215 220

Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile  
 225 230 235 240  
 Asn Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn  
 245 250 255  
 Thr Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu  
 260 265 270  
 Glu Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln  
 275 280 285  
 Pro Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly  
 290 295 300  
 Ala Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala  
 305 310 315 320  
 Gln Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe  
 325 330 335  
 Thr Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly  
 340 345 350  
 Glu Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys  
 355 360 365

<210> 59  
 <211> 1098  
 <212> DNA  
 <213> Artificial Sequence

<400> 59  
 atgggcaaaa tcgttctggt tctgtatgac gctggtaaac acgctgctga cgaagaaaaa 60  
 ctgtacgggt gcaccgaaaa caaactgggt atcgctaact ggctgaaaga tcagggtcac 120  
 gaactgatca ctacctctga caaagaaggt gaaacctctg aactggacaa acacatccccg 180  
 gatgcagata tcatcatcac cactccgttc caccggctt acatcaccaa agagcgtctg 240  
 gacaaagcta aaaacctgaa actggtagta gttgctggtg taggttctga ccacatcgac 300  
 ctggactaca tcaaccagac tggtaaaaaa atctctgtac tggaagtaac tggttctaac 360  
 gttgtttctg ttgctgaaca cgttgtaatg actatgctgg ttctggttcg taacttcggt 420  
 ccggctcaog aacagatcat caaccacgat tgggaagttg cagcaatcgc taaagacgct 480  
 tatgacatcg aaggcaaaac catcgctact atcggcgctg gccgtatcgg ttaccgtggt 540  
 ctggaacgtc tgctgccgtt caaccgaaa gaactgctgt actacgacta ccaggctctg 600  
 ccgaaagaag cagaggagaa agttggtgct cgccgtgtag agaacatcga agagctggta 660  
 gctcaggctg acatcgttac tgttaacgct ccgctgcacg caggcactaa aggtctgatt 720  
 aacaaagagc tgctgtctaa attcaaaaaa ggtgcatggc tggttaaacac tgcacgtggg 780  
 gctatctgcg ttgctgaaga cgttgctgct gcaactggaat ctggtcagct gcgtgggttac 840

ggtggtgacg tatggtttcc gcagccggct ccgaaagatc acccgtggcg tgatatgcgt 900  
aacaaatatg gcgctggtaa cgcaatgacc ccgcactact ctggtaccac tctggatgct 960  
cagacccggt acgctgaagg tactaaaaac atcctggaat ctttcttcac tggtaaattc 1020  
gactaccgcc cgcaggacat cattctgctg aacgggtgaat atgtaactaa agcttacggc 1080  
aaacacgaca aaaaataa 1098

<210> 60  
<211> 365  
<212> PRT  
<213> Artificial Sequence

<400> 60

Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala  
1 5 10 15  
Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala  
20 25 30  
Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys  
35 40 45  
Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile  
50 55 60  
Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu  
65 70 75 80  
Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser  
85 90 95  
Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser  
100 105 110  
Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val  
115 120 125  
Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu  
130 135 140  
Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala  
145 150 155 160  
Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile  
165 170 175  
Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu  
180 185 190  
Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val  
195 200 205  
Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp  
210 215 220  
Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile



ctgtggcgcg gcttgcatgc gggcaacctg cacaccacgg ccaccgacca ctgctgtttc 960  
 tgcgccgaac agaaagccat gggccgcgac gacttcagtc gcatcccca cggcacccgc 1020  
 ggcatcgaag accgcatggc ggtgctgtgg gatgccggtg tcaacagcgg gcgcctgtcg 1080  
 atgcatgagt tcgttgcgct gacctccacc aacacggcaa aaatcttcaa ccttttccca 1140  
 cgcaagggcg ccatccgcgt ggggtccgac gccgacctgg tgctgtggga cccgcagggc 1200  
 actcgcactc tatcggecca gaccacacac cagcgggtgg acttcaatat ctttgaaggc 1260  
 cgcactgtgc gcgggggtccc cagccacacc atcagccagg gcaaggtgct ctgggccgat 1320  
 ggcgacctgc gtcgccgagg ccggggcggg gcggtatgtg gaacggccgg cgtatccgtc 1380  
 ggtgtacgag gtgctggggc gacgcgccga acagcagcgc ccgacgcccg ttcagcgtg 1440  
 aggccattgg ggctgctgcg cagcccatcg ccggcaagcc aaatataa 1488

<210> 62  
 <211> 495  
 <212> PRT  
 <213> Pseudomonas putida

<400> 62

Met Ser Leu Leu Ile Arg Gly Ala Thr Val Val Thr His Glu Glu Ser  
 1 5 10 15  
 Tyr Pro Ala Asp Val Leu Cys Val Asp Gly Leu Ile Arg Ala Ile Gly  
 20 25 30  
 Pro Asn Leu Glu Pro Pro Thr Asp Cys Glu Ile Leu Asp Gly Ser Gly  
 35 40 45  
 Gln Tyr Leu Met Pro Gly Gly Ile Asp Pro His Thr His Met Gln Leu  
 50 55 60  
 Pro Phe Met Gly Thr Val Ala Ser Glu Asp Phe Phe Ser Gly Thr Ala  
 65 70 75 80  
 Ala Gly Leu Ala Gly Gly Thr Thr Ser Ile Ile Asp Phe Val Ile Pro  
 85 90 95  
 Asn Pro Gln Gln Ser Leu Leu Glu Ala Phe His Thr Trp Arg Gly Trp  
 100 105 110  
 Ala Gln Lys Ser Ala Ser Asp Tyr Gly Phe His Val Ala Ile Thr Trp  
 115 120 125  
 Trp Ser Glu Gln Val Ala Glu Glu Met Gly Glu Leu Val Ala Lys His  
 130 135 140  
 Gly Val Asn Ser Phe Lys His Phe Met Ala Tyr Lys Asn Ala Ile Met  
 145 150 155 160  
 Ala Ala Asp Asp Thr Leu Val Ala Ser Phe Glu Arg Cys Leu Gln Leu  
 165 170 175

Gly	Ala	Val	Pro	Thr	Val	His	Ala	Glu	Asn	Gly	Glu	Leu	Val	Tyr	His	180	185	190
Leu	Gln	Lys	Lys	Leu	Leu	Ala	Gln	Gly	Met	Thr	Gly	Pro	Glu	Ala	His	195	200	205
Pro	Leu	Ser	Arg	Pro	Ser	Gln	Val	Glu	Gly	Glu	Ala	Ala	Ser	Arg	Ala	210	215	220
Ile	Arg	Ile	Ala	Glu	Thr	Ile	Gly	Thr	Pro	Leu	Tyr	Val	Val	His	Ile	225	230	235
Ser	Ser	Arg	Glu	Ala	Leu	Asp	Glu	Ile	Thr	Tyr	Ala	Arg	Ala	Lys	Gly	245	250	255
Gln	Pro	Val	Tyr	Gly	Glu	Val	Leu	Pro	Gly	His	Leu	Leu	Leu	Asp	Asp	260	265	270
Ser	Val	Tyr	Arg	Asp	Pro	Asp	Trp	Ala	Thr	Ala	Ala	Gly	Tyr	Val	Met	275	280	285
Ser	Pro	Pro	Phe	Arg	Pro	Arg	Glu	His	Gln	Glu	Ala	Leu	Trp	Arg	Gly	290	295	300
Leu	Gln	Ser	Gly	Asn	Leu	His	Thr	Thr	Ala	Thr	Asp	His	Cys	Cys	Phe	305	310	315
Cys	Ala	Glu	Gln	Lys	Ala	Met	Gly	Arg	Asp	Asp	Phe	Ser	Arg	Ile	Pro	325	330	335
Asn	Gly	Thr	Ala	Gly	Ile	Glu	Asp	Arg	Met	Ala	Val	Leu	Trp	Asp	Ala	340	345	350
Gly	Val	Asn	Ser	Gly	Arg	Leu	Ser	Met	His	Glu	Phe	Val	Ala	Leu	Thr	355	360	365
Ser	Thr	Asn	Thr	Ala	Lys	Ile	Phe	Asn	Leu	Phe	Pro	Arg	Lys	Gly	Ala	370	375	380
Ile	Arg	Val	Gly	Ala	Asp	Ala	Asp	Leu	Val	Leu	Trp	Asp	Pro	Gln	Gly	385	390	395
Thr	Arg	Thr	Leu	Ser	Ala	Gln	Thr	His	His	Gln	Arg	Val	Asp	Phe	Asn	405	410	415
Ile	Phe	Glu	Gly	Arg	Thr	Val	Arg	Gly	Val	Pro	Ser	His	Thr	Ile	Ser	420	425	430
Gln	Gly	Lys	Val	Leu	Trp	Ala	Asp	Gly	Asp	Leu	Arg	Arg	Arg	Gly	Arg	435	440	445
Gly	Gly	Ala	Val	Cys	Gly	Thr	Ala	Gly	Val	Ser	Val	Gly	Val	Arg	Gly	450	455	460
Ala	Gly	Ala	Thr	Arg	Arg	Thr	Ala	Ala	Pro	Asp	Ala	Arg	Ser	Ala	Leu	465	470	475
Arg	Pro	Leu	Gly	Leu	Leu	Arg	Ser	Pro	Ser	Pro	Ala	Ser	Gln	Ile		485	490	495



<210> 63  
 <211> 1491  
 <212> DNA  
 <213> Artificial Sequence

<400> 63  
 atgggctctc tgctgatccg tgggtgctacc gttggttacc acgaagaatc ttatccggct 60  
 gacgtttctgt gcggttgacgg tctgatccgt gctatcggtc cgaacctgga accgccgacc 120  
 gactgcgaaa tcttggaacgg ttctgggtcag tacctgatgc cgggtgggtat cgaccgcgat 180  
 actcacatgc agctgcggtt tatgggtact gttgcttctg aagacttctt ctctggcacc 240  
 gctgctgggc tggtgggtgg taccacctct atcatcgact tcgttatccc gaaccgcgag 300  
 cagtctctgc tggaagcttt ccataacttg cgtggttggg ctcagaaatc tgcactctgac 360  
 tacggtttcc acgttgctat cacctgggtg tctgaacagg ttgctgaaga aatgggagaa 420  
 ctggttgcta aacacggtgt taactcttcc aaacacttca tggcttaca aaacgcaatt 480  
 atggcggctg acgacactct ggttgcttct ttcgaacgct gtctgcagct gggcgctgtt 540  
 ccgaccgttc acgtgaaaaa cggcgagctg gtttatcacc tgcagaaaaa actgctggct 600  
 cagggtatga ctggcccggg agctcaccgc ctgtctcgct cgtctcaggt tgagggcgaa 660  
 gctgcttctc gtgctatccg tatcgctgaa accatcggtt ccccgctgta ttagttcat 720  
 atctcttctc gtgaagctct ggatgagatt acttacgcac gtgctaaggg tcagccggtt 780  
 tacggtgaag ttctgcgggg tcatctgctg ctggatgatt ctgtataccg cgatccggac 840  
 tgggcaactg ctgctgggta cgttatgtcc ccgccgttcc gtccgcgtga gcatcaggag 900  
 gcaactgtggc ggggctgca gtctggtaac ctgcatacta ctgctactga tcaactgtgt 960  
 ttctgcgctg agcagaaggc tatgggtcgc gatgacttct ctgcattcc gaacggtact 1020  
 gctggcattg aggaccgtat ggctgttctg tgggatgctg gcgttaactc tggctgctctg 1080  
 tctatgcacg aattcggttc tctgacctct actaacactg ctaaaatctt caacctgttc 1140  
 ccgcgtaaag gtgcaatccg cgtaggtgca gatgctgac tggttctgtg ggatccgcag 1200  
 ggcactcgca ctctgtctgc tcagactcat catcagcgtg ttgacttcaa catctttgag 1260  
 ggccgtactg ttgcgggtgt tccgtctcat accatctctc agggtaaagt tctgtgggct 1320  
 gacggtgacc tgcgtcgctg tggctggtg ggtgctgttt gcggtagcgc tgggtgtttct 1380  
 gttggtgttc gtggcgctgg tgctaccgct cgtactgctg ctccggatgc tcgttctgct 1440  
 ctgcgtccgc tgggtctgct gcgttctccg tctccggtt ctcagattta a 1491

<210> 64  
 <211> 496  
 <212> PRT  
 <213> Artificial Sequence

[illegible]

44

305		310		315		320
Phe Cys Ala Glu Gln Lys Ala Met Gly Arg Asp Asp Phe Ser Arg Ile						
		325		330		335
Pro Asn Gly Thr Ala Gly Ile Glu Asp Arg Met Ala Val Leu Trp Asp						
		340		345		350
Ala Gly Val Asn Ser Gly Arg Leu Ser Met His Glu Phe Val Ala Leu						
		355		360		365
Thr Ser Thr Asn Thr Ala Lys Ile Phe Asn Leu Phe Pro Arg Lys Gly						
		370		375		380
Ala Ile Arg Val Gly Ala Asp Ala Asp Leu Val Leu Trp Asp Pro Gln						
		385		390		395
Gly Thr Arg Thr Leu Ser Ala Gln Thr His His Gln Arg Val Asp Phe						
		405		410		415
Asn Ile Phe Glu Gly Arg Thr Val Arg Gly Val Pro Ser His Thr Ile						
		420		425		430
Ser Gln Gly Lys Val Leu Trp Ala Asp Gly Asp Leu Arg Arg Arg Gly						
		435		440		445
Arg Gly Gly Ala Val Cys Gly Thr Ala Gly Val Ser Val Gly Val Arg						
		450		455		460
Gly Ala Gly Ala Thr Arg Arg Thr Ala Ala Pro Asp Ala Arg Ser Ala						
		465		470		475
Leu Arg Pro Leu Gly Leu Leu Arg Ser Pro Ser Pro Ala Ser Gln Ile						
		485		490		495

<210> 65  
 <211> 1683  
 <212> DNA  
 <213> Penicillium simplicissimum

<400> 65	
atgtccaaga cacaggaatt caggcctttg acactgccac ccaagctgtc gttaagtgc	60
ttcaatgaat tcatccagga tattattcga atcgttggct ctgaaaatgt tgaagtcatt	120
agctcgaagg accagattgt tgacggttct tatatgaaac ctacgcacac gcacgatccc	180
catcatgtca tggaccagga ctacttcctt gcctcagcaa ttgttgctcc tcgcaatgtc	240
gccgatgtgc agtcgattgt cggacttgcc aataagttct catttcccct ctggcccac	300
tctattggaa gaaattccgg atatggcggg gctgcgccac gggttagtgg cagtgtcgtg	360
ctggacatgg gaaagaatat gaacagagtt ctagaagtga acgtggaagg cgcatattgc	420
gtggtggagc ccggtgtaac ttaccacgac ttgcataatt accttgaggc gaacaatctt	480
cgagacaaat tatggcttga tgtaccggat cttggtggcg gttctgttct cggcaatgcc	540
gttgagagag gtgtgggcta tacgccttac ggagatcatt ggatgatgca cagtgggatg	600

gaagtcgtcc ttgcgaatgg cgagcttctt aggactggca tgggggctct acctgatcct 660  
 aaacgtcccg aaacgatggg gctaaagcca gaagaccagc catggagcaa aatcgctcat 720  
 ctgtttcctt atggcttcgg tccctatata gatgggctat tcagccaatc gaatatggga 780  
 attgttacca agatcgggat ctgggtaatg cccaatccag ggggttatca atcctacttg 840  
 atcacactac ccaaagatgg tgatttaaaa caagccgtcg atattattcg tccccttcgt 900  
 ctaggcacatg cccttcaaaa tgttcccact attcgccaca ttcttttgga tgcagcgggtg 960  
 ctcggtgaca agcgatctta ttcattccaag accgaacccc tctccgacga ggaattagac 1020  
 aagatcgoga aacagctcaa cttgggaaga tggaactttt acggggcgct ctatggacct 1080  
 gagccgattc gaaggggtct ctgggaaacg attaaagacg cattctcggc gatcccaggc 1140  
 gtcaagtttt attttcogga ggacactcct gaaaactccg ttctccgcgt gcgtgataag 1200  
 actatgcaag gcattccaac ttacgacgag ctaaagtgga tcgattggct ccctaattgg 1260  
 ggcacatctg ttttctctcc tattgcaag gtatctggtg aagatgcaat gatgcaatac 1320  
 gcagtcacca agaaaagggtg tcaggagggt gggtagatt ttatcggcac tttcacagtc 1380  
 ggtatgagag agatgcatca tatcgtttgt attgtgttca acaagaagga cctaatacaa 1440  
 aagagaaaag tacagtggct gatgagaacc cttattgatg actgtgctgc aaatggatgg 1500  
 ggogaatatc gaacccatct ggccttcacg gaccaaatta tggaaaccta caactggaac 1560  
 aacagcagct tctaagggtt caatgaggtc ctcaagaatg cgtgggatcc taatggcatc 1620  
 attgccccgg gaaagtctgg tgtttggccg agtcaatata gtcattgttac ttggaaactg 1680  
 taa 1683

<210> 66  
 <211> 560  
 <212> PRT  
 <213> *Penicillium simplicissimum*

<400> 66

Met	Ser	Lys	Thr	Gln	Glu	Phe	Arg	Pro	Leu	Thr	Leu	Pro	Pro	Lys	Leu
1				5					10					15	
Ser	Leu	Ser	Asp	Phe	Asn	Glu	Phe	Ile	Gln	Asp	Ile	Ile	Arg	Ile	Val
			20					25					30		
Gly	Ser	Glu	Asn	Val	Glu	Val	Ile	Ser	Ser	Lys	Asp	Gln	Ile	Val	Asp
		35				40						45			
Gly	Ser	Tyr	Met	Lys	Pro	Thr	His	Thr	His	Asp	Pro	His	His	Val	Met
	50					55				60					
Asp	Gln	Asp	Tyr	Phe	Leu	Ala	Ser	Ala	Ile	Val	Ala	Pro	Arg	Asn	Val
65					70					75				80	



405	410	415
Leu Pro Asn Gly Ala His Leu Phe Phe Ser Pro Ile Ala Lys Val Ser		
420	425	430
Gly Glu Asp Ala Met Met Gln Tyr Ala Val Thr Lys Lys Arg Cys Gln		
435	440	445
Glu Ala Gly Leu Asp Phe Ile Gly Thr Phe Thr Val Gly Met Arg Glu		
450	455	460
Met His His Ile Val Cys Ile Val Phe Asn Lys Lys Asp Leu Ile Gln		
465	470	480
Lys Arg Lys Val Gln Trp Leu Met Arg Thr Leu Ile Asp Asp Cys Ala		
485	490	495
Ala Asn Gly Trp Gly Glu Tyr Arg Thr His Leu Ala Phe Met Asp Gln		
500	505	510
Ile Met Glu Thr Tyr Asn Trp Asn Asn Ser Ser Phe Leu Arg Phe Asn		
515	520	525
Glu Val Leu Lys Asn Ala Val Asp Pro Asn Gly Ile Ile Ala Pro Gly		
530	535	540
Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys Leu		
545	550	555
		560

<210> 67  
 <211> 1686  
 <212> DNA  
 <213> Artificial Sequence

<400> 67  
 atggggtcta aaactcagga gttccgtccg ctgaccctgc cgccgaaact gtctctgtct 60  
 gattttaacg aattcatcca ggatatcatc cgtatcggtg gttctgaaaa cggtgaagtt 120  
 atctcttcta aagaccagat cggtgacggt tcttacatga aaccgaccca caccacgac 180  
 ccgcaccacg ttatggacca ggactacttc ctggcttctg ctatcggtgc tccgcgtaac 240  
 gttgctgacg ttcagtctat cggtggtctg gctaacaaat tctctttccc gctgtggccg 300  
 atctctatcg gtcgtaactc tggttacggt ggtgctgctc cgcgtgtttc tggttctggt 360  
 gttctggaca tgggtaaaaa catgaaccgt gttctggaag ttaacgttga aggtgcttac 420  
 tgcgttggtg aaccgggtgt aacttatcat gacctgcaca actacctgga agctaacaac 480  
 ctgcgtgaca aactgtggct ggacgtaccg gatctgggtg gtggttctgt tctgggtaac 540  
 gctgttgaaac gtggtggttg ttacaccccg tacggtgac attggatgat gcactctggc 600  
 atggaggtag tactggctaa cggtgaaactg ctgcgtaccg gtatgggtgc tctgccggac 660  
 ccgaagcgtc cggaactat gggctctgaag ccggaggatc agccgtggtc taaaatcgct 720  
 catctgttcc cgtatggctt tggccgtac atcgacggtc tgttctctca gtctaacatg 780

```

ggatcgtta ccaaaattgg catttggctg atgccgaacc cgggtgggta ccagtcttac      840
ctgattactc tgccgaaaga tggcgacctg aaacaggctg ttgatatcat tcgcccgtg      900
cgtctgggta tggctctgca gaacgttccg actatccgcc acatcctgct ggacgtgca      960
gtactgggtg acaaacgttc ctactcctct aaaactgaac cgctgtctga cgaagaactg     1020
gacaaaatcg ctaaacagct gaacctgggt cgttggaact tctacggtgc tctgtacggt     1080
ccggaaccga tccgtcgtgt tctgtgggag actatcaagg atgctttctc tgctatcccg     1140
ggtgttaa at tctacttccc ggaagacact ccgaaaaact ctgttctgcg tgtacgtgac     1200
aaaaccatgc agggtatccc gacctacgac gaactgaaat ggatcgactg gctgccgaac     1260
ggtgctcacc tgttcttttc tccgatcgct aaagtatccg gagaggacgc tatgatgcag     1320
tatgctgtta ccaaaaaacg ttgtcaggaa gctgggtctgg atttcattgg taccttcaact     1380
gtaggtatgc gcgaaatgca tcatattgtt tgcacggtt tcaacaaaaa agacctgatt     1440
cagaagcgca aagttcagtg gctgatgcgt accctgatcg acgactgtgc tgctaacggt     1500
tgggggtgaat accgtaccca cctggcattc atggaccaga tcatggaaac ctacaactgg     1560
aacaactctt ctttctgcg tttcaacgaa gttctgaaaa acgctgttga cccgaacggt     1620
atcatcgctc cgggtaaate tgggtgttgg ccgtctcagt actctcacgt tacctggaaa     1680
ctgtaa                                                                    1686

```

```

<210> 68
<211> 561
<212> PRT
<213> Artificial Sequence

```

```

<400> 68

```

```

Met Gly Ser Lys Thr Gln Glu Phe Arg Pro Leu Thr Leu Pro Pro Lys
1          5          10          15
Leu Ser Leu Ser Asp Phe Asn Glu Phe Ile Gln Asp Ile Ile Arg Ile
20        25        30
Val Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val
35        40        45
Asp Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val
50        55        60
Met Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn
65        70        75        80
Val Ala Asp Val Gln Ser Ile Val Gly Leu Ala Asn Lys Phe Ser Phe
85        90        95
Pro Leu Trp Pro Ile Ser Ile Gly Arg Asn Ser Gly Tyr Gly Gly Ala
100       105       110

```

Ala Pro Arg Val Ser Gly Ser Val Val Leu Asp Met Gly Lys Asn Met  
115 120 125

Asn Arg Val Leu Glu Val Asn Val Glu Gly Ala Tyr Cys Val Val Glu  
130 135 140

Pro Gly Val Thr Tyr His Asp Leu His Asn Tyr Leu Glu Ala Asn Asn  
145 150 155 160

Leu Arg Asp Lys Leu Trp Leu Asp Val Pro Asp Leu Gly Gly Gly Ser  
165 170 175

Val Leu Gly Asn Ala Val Glu Arg Gly Val Gly Tyr Thr Pro Tyr Gly  
180 185 190

Asp His Trp Met Met His Ser Gly Met Glu Val Val Leu Ala Asn Gly  
195 200 205

Glu Leu Leu Arg Thr Gly Met Gly Ala Leu Pro Asp Pro Lys Arg Pro  
210 215 220

Glu Thr Met Gly Leu Lys Pro Glu Asp Gln Pro Trp Ser Lys Ile Ala  
225 230 235 240

His Leu Phe Pro Tyr Gly Phe Gly Pro Tyr Ile Asp Gly Leu Phe Ser  
245 250 255

Gln Ser Asn Met Gly Ile Val Thr Lys Ile Gly Ile Trp Leu Met Pro  
260 265 270

Asn Pro Gly Gly Tyr Gln Ser Tyr Leu Ile Thr Leu Pro Lys Asp Gly  
275 280 285

Asp Leu Lys Gln Ala Val Asp Ile Ile Arg Pro Leu Arg Leu Gly Met  
290 295 300

Ala Leu Gln Asn Val Pro Thr Ile Arg His Ile Leu Leu Asp Ala Ala  
305 310 315 320

Val Leu Gly Asp Lys Arg Ser Tyr Ser Ser Lys Thr Glu Pro Leu Ser  
325 330 335

Asp Glu Glu Leu Asp Lys Ile Ala Lys Gln Leu Asn Leu Gly Arg Trp  
340 345 350

Asn Phe Tyr Gly Ala Leu Tyr Gly Pro Glu Pro Ile Arg Arg Val Leu  
355 360 365

Trp Glu Thr Ile Lys Asp Ala Phe Ser Ala Ile Pro Gly Val Lys Phe  
370 375 380

Tyr Phe Pro Glu Asp Thr Pro Glu Asn Ser Val Leu Arg Val Arg Asp  
385 390 395 400

Lys Thr Met Gln Gly Ile Pro Thr Tyr Asp Glu Leu Lys Trp Ile Asp  
405 410 415

Trp Leu Pro Asn Gly Ala His Leu Phe Phe Ser Pro Ile Ala Lys Val  
420 425 430

Ser Gly Glu Asp Ala Met Met Gln Tyr Ala Val Thr Lys Lys Arg Cys





<210> 70  
 <211> 283  
 <212> PRT  
 <213> Candida magnoliae

<400> 70

Met	Ala	Lys	Asn	Phe	Ser	Asn	Val	Glu	Tyr	Pro	Ala	Pro	Pro	Pro	Ala	
1			5						10						15	
His	Thr	Lys	Asn	Glu	Ser	Leu	Gln	Val	Leu	Asp	Leu	Phe	Lys	Leu	Asn	
			20					25					30			
Gly	Lys	Val	Ala	Ser	Ile	Thr	Gly	Ser	Ser	Ser	Gly	Ile	Gly	Tyr	Ala	
		35					40					45				
Leu	Ala	Glu	Ala	Phe	Ala	Gln	Val	Gly	Ala	Asp	Val	Ala	Ile	Trp	Tyr	
	50					55					60					
Asn	Ser	His	Asp	Ala	Thr	Gly	Lys	Ala	Glu	Ala	Leu	Ala	Lys	Lys	Tyr	
65					70					75					80	
Gly	Val	Lys	Val	Lys	Ala	Tyr	Lys	Ala	Asn	Val	Ser	Ser	Ser	Asp	Ala	
			85						90					95		
Val	Lys	Gln	Thr	Ile	Glu	Gln	Gln	Ile	Lys	Asp	Phe	Gly	His	Leu	Asp	
			100					105					110			
Ile	Val	Val	Ala	Asn	Ala	Gly	Ile	Pro	Trp	Thr	Lys	Gly	Ala	Tyr	Ile	
	115						120					125				
Asp	Gln	Asp	Asp	Asp	Lys	His	Phe	Asp	Gln	Val	Val	Asp	Val	Asp	Leu	
	130					135					140					
Lys	Gly	Val	Gly	Tyr	Val	Ala	Lys	His	Ala	Gly	Arg	His	Phe	Arg	Glu	
145					150					155					160	
Arg	Phe	Glu	Lys	Glu	Gly	Lys	Lys	Gly	Ala	Leu	Val	Phe	Thr	Ala	Ser	
				165					170					175		
Met	Ser	Gly	His	Ile	Val	Asn	Val	Pro	Gln	Phe	Gln	Ala	Thr	Tyr	Asn	
			180					185					190			
Ala	Ala	Lys	Ala	Gly	Val	Arg	His	Phe	Ala	Lys	Ser	Leu	Ala	Val	Glu	
		195				200						205				
Phe	Ala	Pro	Phe	Ala	Arg	Val	Asn	Ser	Val	Ser	Pro	Gly	Tyr	Ile	Asn	
	210					215					220					
Thr	Glu	Ile	Ser	Asp	Phe	Val	Pro	Gln	Glu	Thr	Gln	Asn	Lys	Trp	Trp	
225					230					235				240		
Ser	Leu	Val	Pro	Leu	Gly	Arg	Gly	Gly	Glu	Thr	Ala	Glu	Leu	Val	Gly	
				245					250					255		
Ala	Tyr	Leu	Phe	Leu	Ala	Ser	Asp	Ala	Gly	Ser	Tyr	Ala	Thr	Gly	Thr	
		260						265					270			
Asp	Ile	Ile	Val	Asp	Gly	Gly	Tyr	Thr	Leu	Pro						

```
<210> 71
<211> 852
<212> DNA
<213> Artificial Sequence
```

<400>	71						
atgggctaaaa	acttctctaa	cgttgaatac	ccggctccgc	cgccagctca	caccaaaaaac		60
gaatctctgc	aggttctgga	cctgttcaaa	ctgaacggta	aggttgcttc	tatcacccgt		120
tcttctcttg	gratcgggta	cgtctctggc	gaagcattcg	ctcaggtagg	tgtcgacgtt		180
gcratctcgt	acaactctca	cgacgctact	ggtaaggctg	aagctctggc	taaaaaatac		240
ggtgttaaag	ttaaagctta	caaggctaac	gtttcttctt	ctgacgctgt	aaaacagacc		300
atcgaacagc	agatcaaaga	cttcggtcac	ctggacatcg	ttgttgctaa	cgctgggtatc		360
ccgtggacca	aagggtgctta	catcgaccag	gacgacgata	aacacttcga	tcagggttggt		420
gacgttgatc	tgaaagggtg	tggttatggt	gctaaacacg	ctggccgctca	cttccgtgag		480
cgtttcgaaa	aggaaggtaa	gaaaggcgct	ctggttttca	ccgcttctat	gtctgggtcac		540
atcgttaacg	taccgcagtt	tcaggctacc	tacaacgctg	ctaaagctgg	tgttcgtcac		600
ttcgctaaat	ctctggctgt	agaattcgct	ccgttcgctc	gtgttaactc	tgtttctccg		660
ggctacatca	acaccgaaat	ctctgacttt	gtaccgcagg	aaactcagaa	caaatggtgg		720
tctctggtac	cgctggggccg	tgggtggcgaa	actgctgaac	tggttggtgc	ttacctgttt		780
ctggcttctg	acgctgggtc	ttacgctacc	ggcactgaca	tcacgttgga	cggtgggttac		840
acctgcccgt	aa						852

```
<210> 72
<211> 1602
<212> DNA
<213> Saccharomyces cerevisiae
```

<400>	72						
atgacagaag	ataatattgc	tccaatcacc	tccgttaaag	tagttacoga	caagtgcacg		60
tacaaggaca	acgagctgct	caccaagtac	agctacgaaa	atgctgtagt	tacgaagaca		120
gctagtggcc	gcttcgatgt	aacgcccact	gttcaagaact	acgtgttcaa	aottgacttg		180
aaaaagccgg	aaaaactagg	aattatgctc	attgggttag	gtggcaacaa	tggctccact		240
ttagtggcct	cggtattggc	gaataagcac	aatgtggagt	ttcaaaactaa	ggaaggcggt		300
aagcaaccaa	actacttcgg	ctccatgact	caatgttcta	cottgaaact	gggtatcgat		360
gcggagggga	atgacgttta	tgctcctttt	aactctctgt	tgcccatggt	tagcccaaac		420
gactttgtcg	tctctggttg	ggacatcaat	aacgcagatc	tatacgaagc	tatgcagaga		480

agtcaagttc tcgaatatga tctgcaacaa cgcttgaagg cgaagatgtc cttggtgaag 540  
cctcttcctt ccatttacta ccctgatttc attgcagcta atcaagatga gagagccaat 600  
aactgcatca atttgatga aaaaggcaac gtaaccacga ggggtaagtg gacccatctg 660  
caacgcatca gacgcgatat ccagaatttc aaagaagaaa acgcccttga taaagtaatc 720  
gttcttttga ctgcaaatac tgagaggtac gtagaagtat ctcttggtgt taatgacacc 780  
atggaaaacc tcttgcatgc tattaagaat gaccatgaag agattgctcc ttccacgac 840  
tttgcatcag catctatctt ggaagggtgc ccctatatta atgggttcacc gcagaatact 900  
tttggtcccg gcttggttca gctggctgag catgagggtta cattcattgc gggagacgat 960  
ctcaagtcgg gacaaaccaa gttgaagtct gttctggccc agttcttagt ggatgcagg 1020  
attaaaccgg tctccattgc atctataaac catttaggca ataagacgg ttataactta 1080  
tctgctccaa aacaatttag gtctaaggag atttccaaaa gttctgtcat agatgacatc 1140  
atcgcttcta atgatatctt gtacaatgat aaactgggta aaaaagttga ccaactgcatt 1200  
gtcatcaa atatgaagcc cgtcggggac tcaaaagtgg caatggacga gtattacagt 1260  
gagttgatgt taggtggcca taaccggatt tccattcaca atgtttgcga agattcttta 1320  
ctggctacgc ccttgatcat cgatctttta gtcatgactg agttttgtac aagagtgtcc 1380  
tataagaagg tggaccaggt taaagaagat gctggcaaat tcgagaactt ttatccagtt 1440  
ttaaccttct tgagttactg gttaaaagct ccattaacaa gaccaggatt tcaccgggtg 1500  
aatggcttaa acaagcaaag aaccgcctta gaaaattttt taagattggt gattggattg 1560  
ccttctcaaa acgaactaag attcgaagag agattgttgt aa 1602

<210> 73  
<211> 533  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 73

Met	Thr	Glu	Asp	Asn	Ile	Ala	Pro	Ile	Thr	Ser	Val	Lys	Val	Val	Thr
1				5					10					15	
Asp	Lys	Cys	Thr	Tyr	Lys	Asp	Asn	Glu	Leu	Leu	Thr	Lys	Tyr	Ser	Tyr
			20					25					30		
Glu	Asn	Ala	Val	Val	Thr	Lys	Thr	Ala	Ser	Gly	Arg	Phe	Asp	Val	Thr
			35				40					45			
Pro	Thr	Val	Gln	Asp	Tyr	Val	Phe	Lys	Leu	Asp	Leu	Lys	Lys	Pro	Glu
	50					55					60				
Lys	Leu	Gly	Ile	Met	Leu	Ile	Gly	Leu	Gly	Gly	Asn	Asn	Gly	Ser	Thr
65					70				75					80	



405	410	415
Glu Tyr Tyr Ser Glu Leu Met Leu Gly Gly His Asn Arg Ile Ser Ile 420 425 430		
His Asn Val Cys Glu Asp Ser Leu Leu Ala Thr Pro Leu Ile Ile Asp 435 440 445		
Leu Leu Val Met Thr Glu Phe Cys Thr Arg Val Ser Tyr Lys Lys Val 450 455 460		
Asp Pro Val Lys Glu Asp Ala Gly Lys Phe Glu Asn Phe Tyr Pro Val 465 470 475 480		
Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro Gly 485 490 495		
Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu Asn 500 505 510		
Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg Phe 515 520 525		
Glu Glu Arg Leu Leu 530		

<210> 74  
 <211> 1605  
 <212> DNA  
 <213> Artificial Sequence

<400> 74  
 atgggtaccg aagataacat cgctccaatc acttctgtta aagttgtaac tgacaaatgt 60  
 acttacaaag acaacgaact gctgactaaa tactcttacg aaaacgctgt agtaactaaa 120  
 actgcttctg gtcgtttcga tgttactccg actgttcagg actacgtatt caaactggat 180  
 ctgaagaaac cggaaaagct gggatatcatg ctgatcggcc tgggtggtaa caacggctct 240  
 actctgggtg catctgttct ggcaaacaaa cacaacgtag aattccagac taaggaaggt 300  
 gttaaacagc cgaactactt tggttctatg actcagtgtt ctactctgaa gctgggcatt 360  
 gatgctgaag gtaacgacgt ttacgctccg ttcaactctc tgctgccgat ggtatctccg 420  
 aacgacttcg ttgtttctgg ttgggatatc aacaacgcgg atctgtacga agcaatgcag 480  
 cgttctcagg ttctggaata tgatctgcaa cagcgtctga aggctaagat gtctctgggt 540  
 aagccactgc cgtccatcta ctaccggat tttatcgcag ctaaccagga cgaacgtgct 600  
 aacaactgta tcaacctgga cgaaaagggg aacgttacta cccgtggtaa gtggactcac 660  
 ctgcagcgta tccgtcgtga tatccagaac ttcaaagagg aaaacgcact ggacaaagtt 720  
 atcgtactgt ggactgctaa cactgaacgt tacgtagaag tatccccggg tgtaaacgat 780  
 actatggaaa acctgctgca atctatcaag aacgaccacg aggaaatcgc tccgtccacc 840  
 atcttcgctg ctgcatctat cctggaaggc gtaccgtaca tcaacggctc tccgcagaac 900

```

actttcgtac cgggtctggt acagctggct gaacacgaag gtaccttcat cgctggtgac      960
gatctgaaat ctggccagac taaactgaaa tctgtactgg cacagttcct gggtgacgct      1020
ggtatcaaac cggtttctat cgcttcttat aaccacctgg gtaacaacga cggctacaac      1080
ctgtctgctc cgaaacagtt ccgttctaaa gaaatctcta aatcctctgt aatcgacgac      1140
atcatcgctt ctaacgacat cctgtacaac gacaaaactgg gtaagaaagt agatcactgt      1200
atcgttatca aatacatgaa accggttggt gattctaaag ttgctatgga cgaatactac      1260
tctgaactga tgctgggagg tcacaaccgt atctctatcc acaacgtttg tgaagactct      1320
ctgctggcta ccccgctgat catcgacctg ctggttatga ctgaattctg tacccggtga      1380
tcttacaaga aagttgaccc ggtaaagaa gatgctggca aattcgaaaa cttctacccg      1440
gtttctgacct tctgtcttta ctggctgaaa gctccgctga ctggtccagg cttccacccg      1500
gttaacggtc tgaacaaaca gcgtaccgct ctggaaaact tctgctgtct gctgatcggc      1560
ctgcgcgtccc agaacgaact gcgtttcgaa gaacgtctgc tgtaa                        1605

```

```

<210> 75
<211> 534
<212> PRT
<213> Artificial Sequence

```

```
<400> 75
```

```

Met Gly Thr Glu Asp Asn Ile Ala Pro Ile Thr Ser Val Lys Val Val
1          5          10          15

Thr Asp Lys Cys Thr Tyr Lys Asp Asn Glu Leu Leu Thr Lys Tyr Ser
          20          25          30

Tyr Glu Asn Ala Val Val Thr Lys Thr Ala Ser Gly Arg Phe Asp Val
          35          40          45

Thr Pro Thr Val Gln Asp Tyr Val Phe Lys Leu Asp Leu Lys Lys Pro
50          55          60

Glu Lys Leu Gly Ile Met Leu Ile Gly Leu Gly Gly Asn Asn Gly Ser
65          70          75          80

Thr Leu Val Ala Ser Val Leu Ala Asn Lys His Asn Val Glu Phe Gln
          85          90          95

Thr Lys Glu Gly Val Lys Gln Pro Asn Tyr Phe Gly Ser Met Thr Gln
          100         105         110

Cys Ser Thr Leu Lys Leu Gly Ile Asp Ala Glu Gly Asn Asp Val Tyr
          115         120         125

Ala Pro Phe Asn Ser Leu Leu Pro Met Val Ser Pro Asn Asp Phe Val
          130         135         140

Val Ser Gly Trp Asp Ile Asn Asn Ala Asp Leu Tyr Glu Ala Met Gln

```

145		150		155		160
Arg Ser Gln Val	Leu Glu Tyr Asp	Leu Gln Gln Arg	Leu Lys Ala Lys			
	165		170		175	
Met Ser Leu Val	Lys Pro Leu Pro	Ser Ile Tyr Tyr	Pro Asp Phe Ile			
	180	185	190			
Ala Ala Asn Gln	Asp Glu Arg Ala	Asn Asn Cys Ile	Asn Leu Asp Glu			
	195	200	205			
Lys Gly Asn Val	Thr Thr Arg Gly	Lys Trp Thr His	Leu Gln Arg Ile			
	210	215	220			
Arg Arg Asp Ile	Gln Asn Phe Lys	Glu Glu Asn Ala	Leu Asp Lys Val			
225	230	235	240			
Ile Val Leu Trp	Thr Ala Asn Thr	Glu Arg Tyr Val	Glu Val Ser Pro			
	245	250	255			
Gly Val Asn Asp	Thr Met Glu Asn	Leu Leu Gln Ser	Ile Lys Asn Asp			
	260	265	270			
His Glu Glu Ile	Ala Pro Ser Thr	Ile Phe Ala Ala	Ala Ser Ile Leu			
	275	280	285			
Glu Gly Val Pro	Tyr Ile Asn Gly	Ser Pro Gln Asn	Thr Phe Val Pro			
	290	295	300			
Gly Leu Val Gln	Leu Ala Glu His	Glu Gly Thr Phe	Ile Ala Gly Asp			
305	310	315	320			
Asp Leu Lys Ser	Gly Gln Thr Lys	Leu Lys Ser Val	Leu Ala Gln Phe			
	325	330	335			
Leu Val Asp Ala	Gly Ile Lys Pro	Val Ser Ile Ala	Ser Tyr Asn His			
	340	345	350			
Leu Gly Asn Asn	Asp Gly Tyr Asn	Leu Ser Ala Pro	Lys Gln Phe Arg			
	355	360	365			
Ser Lys Glu Ile	Ser Lys Ser Ser	Val Ile Asp Asp	Ile Ile Ala Ser			
370	375	380				
Asn Asp Ile Leu	Tyr Asn Asp Lys	Leu Gly Lys Lys	Val Asp His Cys			
385	390	395	400			
Ile Val Ile Lys	Tyr Met Lys Pro	Val Gly Asp Ser	Lys Val Ala Met			
	405	410	415			
Asp Glu Tyr Tyr	Ser Glu Leu Met	Leu Gly Gly His	Asn Arg Ile Ser			
	420	425	430			
Ile His Asn Val	Cys Glu Asp Ser	Leu Leu Ala Thr	Pro Leu Ile Ile			
	435	440	445			
Asp Leu Leu Val	Met Thr Glu Phe	Cys Thr Arg Val	Ser Tyr Lys Lys			
	450	455	460			
Val Asp Pro Val	Lys Glu Asp Ala	Gly Lys Phe Glu	Asn Phe Tyr Pro			
465	470	475	480			



Val Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro  
 485 490 495  
 Gly Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu  
 500 505 510  
 Asn Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg  
 515 520 525  
 Phe Glu Glu Arg Leu Leu  
 530

<210> 76  
 <211> 2043  
 <212> DNA  
 <213> Hypomyces rosellus

<400> 76  
 atgaaacacc ttttaacact cgctctttgc ttcagcagca tcaatgctgt tgctgtcacc 60  
 gtccctcaca aggccgtagg aactggaatt cctgaaggga gtcttcagtt cctgagcctt 120  
 cgagcctcag cacctatcgg aagcgccatt totcgcaaca actgggcccgt cacttgcgac 180  
 agtgcacagt cgggaaatga atgcaacaag gccattgatg gcaacaagga taccttttgg 240  
 cacacattct atggcgccaa cggggatcca aagccccctc acacatacac gattgacatg 300  
 aagacaactc agaacgtcaa cggcttgtct atgctgcctc gacaggatgg taaccaaacc 360  
 ggctggatcg gtcgcatga ggtttatcta agctcagatg gcacaaactg gggcagccct 420  
 gttgcgtcag gtagttgggt cgccgactct actacaaaat actccaactt tgaaactcgc 480  
 cctgctcgct atgttcgtct tgcgctatc actgaagcga atggccagcc ttggactagc 540  
 attgcagaga tcaacgtctt ccaagctagt tcttacacag cccccagcc tggctttgga 600  
 cgctgggggc cgactattga cttaccgatt gttcctgcgg ctgcagcaat tgaaccgaca 660  
 tcgggacgag tccttatgtg gtcttcatat cgcaatgatg catttgagg atccctgggt 720  
 ggtatcactt tgacgtcttc ctgggatcca tccactggta ttgtttccga cgcactgtg 780  
 acagtcacca agcatgatat gttctgccct ggtatctcca tggatggtaa cggtcagatc 840  
 gtagtcacag gtggcaacga tgccaagaag accagtttgt atgattcatc tagcgatagc 900  
 tggatcccgg gacctgacat gcaagtggct cgtgggtatc agtcatcagc taccatgtca 960  
 gacggtcgtg tttttacat tggaggctcc tggagcgggt gcgtatttga gaagaatggc 1020  
 gaagtctata gcccatcttc aaagacatgg acgtccctac ccaatgcca ggtcaacca 1080  
 atgttgacgg ctgacaagca aggattgtac cgttcagaca accacgcgtg gctctttgga 1140  
 tggaagaagg gttcgggtgtt ccaagcggga cctagcacag ccatgaactg gtactatacc 1200  
 agtggaagtg gtgatgtgaa gtcagccgga aaacgccagt ctaaccgtgg ttagccct 1260

gatgccatgt goggaaaacgc tgtcatgtac gacgccgtta aaggaaagat cctgaccttt 1320  
 ggcggtccc cagattatca agactctgac gccacaacca acgcccacat catcaccctc 1380  
 ggtgaaccog gaacatctcc caacactgtc tttgctagca atgggttgta ctttgcccga 1440  
 acgtttcaca cctctgttgt tottccagac ggaagcacgt ttattacagg aggccaacga 1500  
 cgtggaattc cgttcgagga ttcaaccccg gtatttacac ctgagatcta cgtccctgaa 1560  
 caagacactt tctacaagca gaacccaac tccattgttc gcgtctacca tagcatttcc 1620  
 cttttgttac ctgatggcag ggtatttaac ggtggtggtg gtctttgtgg cgattgtacc 1680  
 acgaatcatt togaogcgca aatctttacg ccaaactatc tttacaatag caacggcaat 1740  
 ctgcgcacac gtcccaagat taccagaacc tctacacaga gcgtcaaggt cggtggcaga 1800  
 attacaatct cgacggattc ttcgattagc aaggcgctgt tgattcgcta tggtagcg 1860  
 acacacacgg ttaatactga ccagcgccgc attcccctga ctctgacaaa caatggagga 1920  
 aatagctatt ctttccaagt toctagcgac tctggtgttg ctttgccctgg ctactggatg 1980  
 ttgttcgtga tgaactcggc cgggtgttct agtgtggctt cgacgattcg cgttactcag 2040  
 tga 2043

<210> 77  
 <211> 680  
 <212> PRT  
 <213> *Hypomyces rosellus*  
 <400> 77

Met	Lys	His	Leu	Leu	Thr	Leu	Ala	Leu	Cys	Phe	Ser	Ser	Ile	Asn	Ala
1			5						10					15	
Val	Ala	Val	Thr	Val	Pro	His	Lys	Ala	Val	Gly	Thr	Gly	Ile	Pro	Glu
			20					25					30		
Gly	Ser	Leu	Gln	Phe	Leu	Ser	Leu	Arg	Ala	Ser	Ala	Pro	Ile	Gly	Ser
		35					40					45			
Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val	Thr	Cys	Asp	Ser	Ala	Gln	Ser
	50					55					60				
Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp	Gly	Asn	Lys	Asp	Thr	Phe	Trp
65				70					75					80	
His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp	Pro	Lys	Pro	Pro	His	Thr	Tyr
				85				90					95		
Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn	Val	Asn	Gly	Leu	Ser	Met	Leu
			100					105					110		
Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly	Trp	Ile	Gly	Arg	His	Glu	Val
		115					120					125			
Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp	Gly	Ser	Pro	Val	Ala	Ser	Gly



Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg  
 465 470 475 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr  
 485 490 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe  
 500 505 510

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn  
 515 520 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro  
 530 535 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr  
 545 550 555 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn  
 565 570 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr  
 580 585 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser  
 595 600 605

Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val  
 610 615 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly  
 625 630 635 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro  
 645 650 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val  
 660 665 670

Ala Ser Thr Ile Arg Val Thr Gln  
 675 680

<210> 78  
 <211> 2046  
 <212> DNA  
 <213> Artificial Sequence

<400> 78  
 atgggcaagc atctgctgac tctggcactg tgtttctctt ctatcaacgc tgttgctgta 60  
 accgttccgc ataaggctgt tggtagcggg atcccgaag gttctctgca gttcctgtct 120  
 ctgctgtgctt ctgctccgat cggttctgct atctctcgta acaactgggc agttacctgc 180  
 gactccgcac agtctggtaa cgaatgcaac aaagctatcg acgtaacaa agacactttt 240  
 tggcacactt tctatggcgc taacggcgac ccgaaaccgc cgcacaccta caccatcgat 300  
 atgaaaacca ctcagaacgt aaacggcctg tctatgctgc cgcgccagga tggttaaccag 360



<212> PRT  
 <213> Artificial Sequence

<400> 79

```

Met Gly Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn
1          5          10          15

Ala Val Ala Val Thr Val Pro His Lys Ala Val Gly Thr Gly Ile Pro
          20          25          30

Glu Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly
          35          40          45

Ser Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln
          50          55          60

Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe
          65          70          75          80

Trp His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr
          85          90          95

Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met
          100          105          110

Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu
          115          120          125

Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp Gly Ser Pro Val Ala Ser
          130          135          140

Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr
          145          150          155          160

Arg Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly
          165          170          175

Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser
          180          185          190

Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp
          195          200          205

Leu Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg
          210          215          220

Val Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro
          225          230          235          240

Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val
          245          250          255

Ser Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly
          260          265          270

Ile Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp
          275          280          285

Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro
          290          295          300
  
```

Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr	Gln	Ser	Ser	Ala	Thr	Met	305	310	315	320
Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly	Ser	Trp	Ser	Gly	Gly	Val	325	330	335	
Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro	Ser	Ser	Lys	Thr	Trp	Thr	340	345	350	
Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met	Leu	Thr	Ala	Asp	Lys	Gln	355	360	365	
Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp	Leu	Phe	Gly	Trp	Lys	Lys	370	375	380	
Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr	Ala	Met	Asn	Trp	Tyr	Tyr	385	390	395	400
Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala	Gly	Lys	Arg	Gln	Ser	Asn	405	410	415	
Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly	Asn	Ala	Val	Met	Tyr	Asp	420	425	430	
Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly	Gly	Ser	Pro	Asp	Tyr	Gln	435	440	445	
Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile	Ile	Thr	Leu	Gly	Glu	Pro	450	455	460	
Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser	Asn	Gly	Leu	Tyr	Phe	Ala	465	470	475	480
Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro	Asp	Gly	Ser	Thr	Phe	Ile	485	490	495	
Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe	Glu	Asp	Ser	Thr	Pro	Val	500	505	510	
Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln	Asp	Thr	Phe	Tyr	Lys	Gln	515	520	525	
Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His	Ser	Ile	Ser	Leu	Leu	Leu	530	535	540	
Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly	Gly	Leu	Cys	Gly	Asp	Cys	545	550	555	560
Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe	Thr	Pro	Asn	Tyr	Leu	Tyr	565	570	575	
Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro	Lys	Ile	Thr	Arg	Thr	Ser	580	585	590	
Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile	Thr	Ile	Ser	Thr	Asp	Ser	595	600	605	
Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr	Gly	Thr	Ala	Thr	His	Thr	610	615	620	

